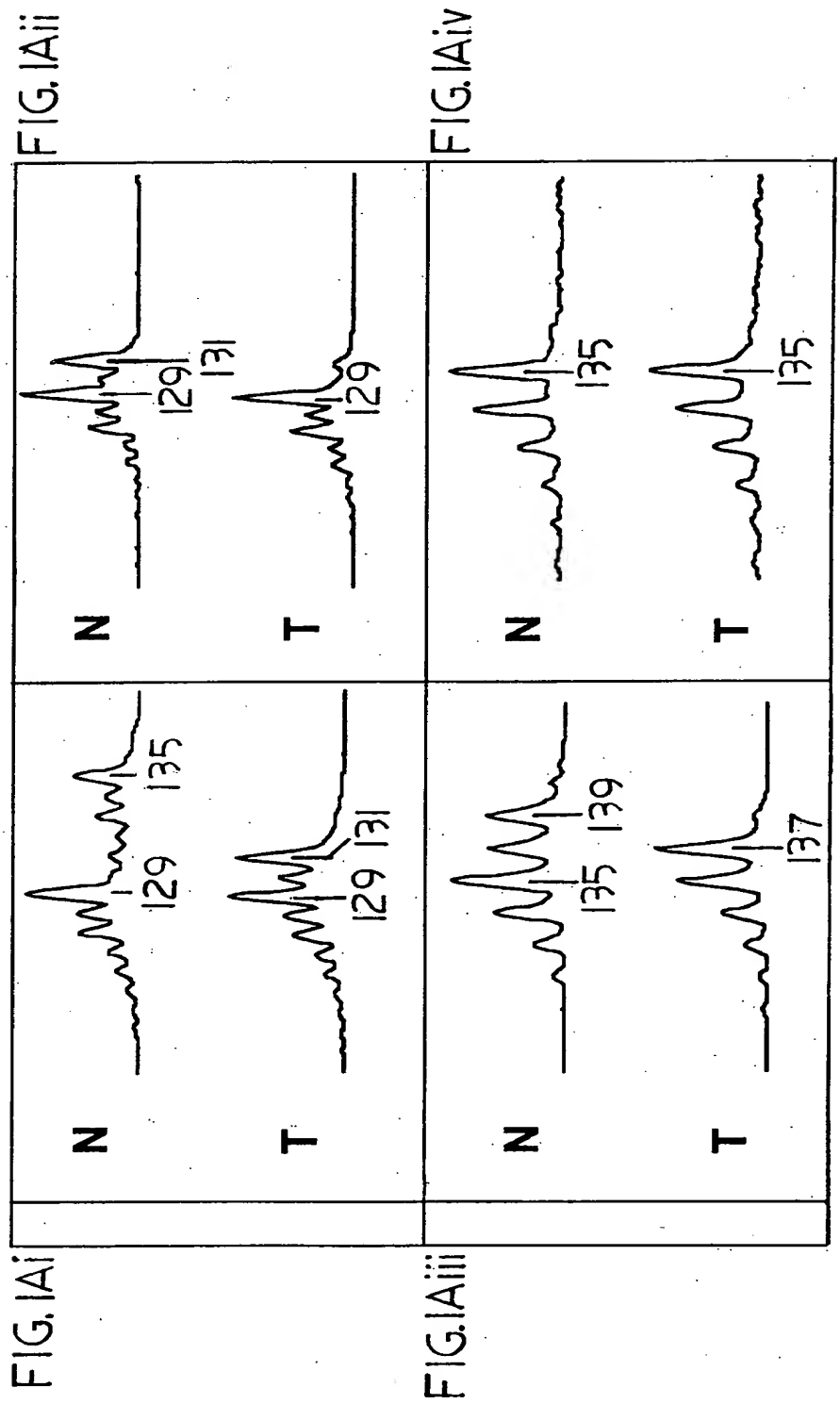
FIG. IAi
N
T
129
135
129
131
FIG. IAii
N
T
129
131
129
FIG. IAiii
N
T
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139
137
FIG. IAiv
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T
135
135

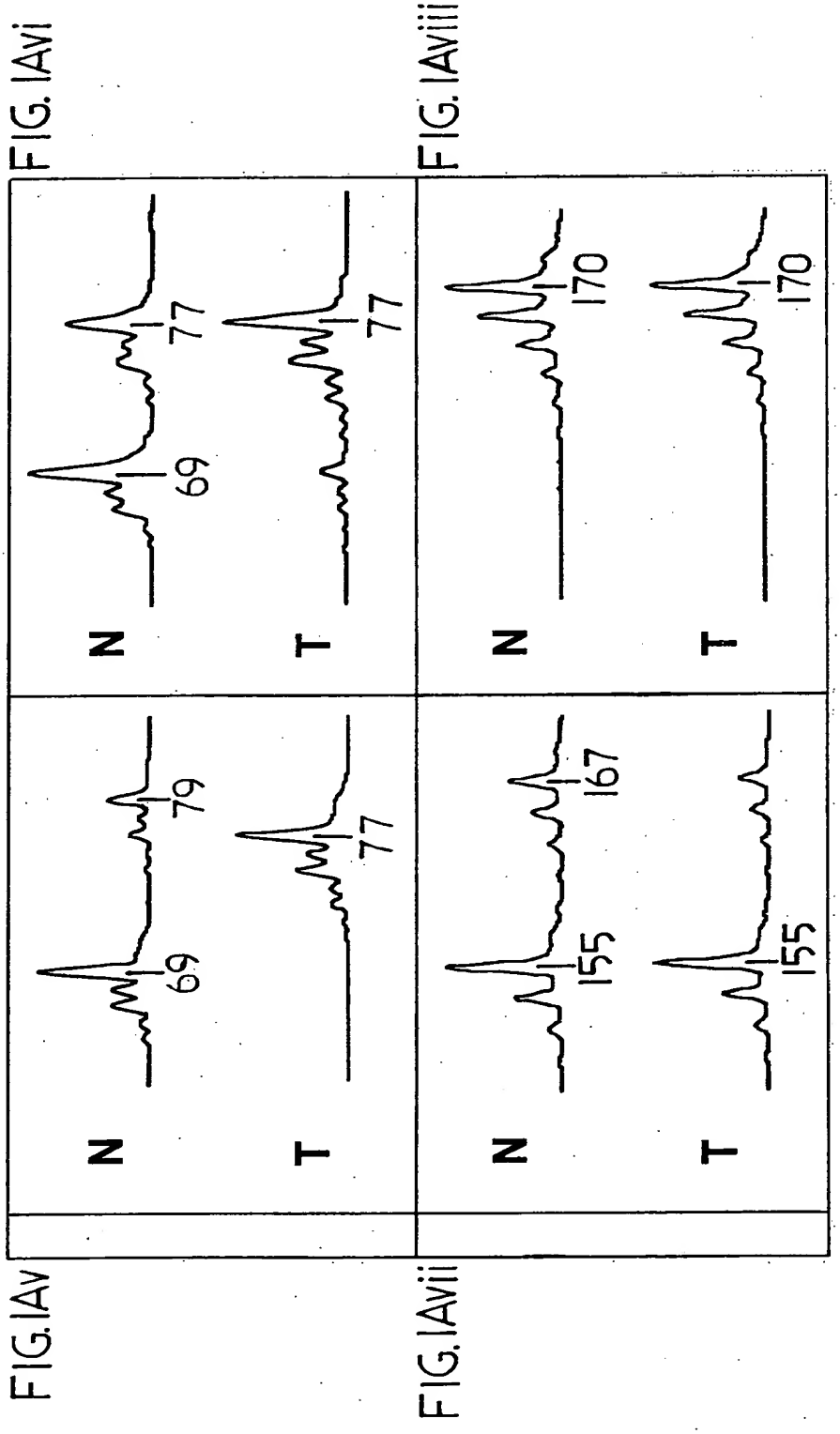
FIG. IAvi
FIG. IAviii
FIG. IAv
FIG. IAvii
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T
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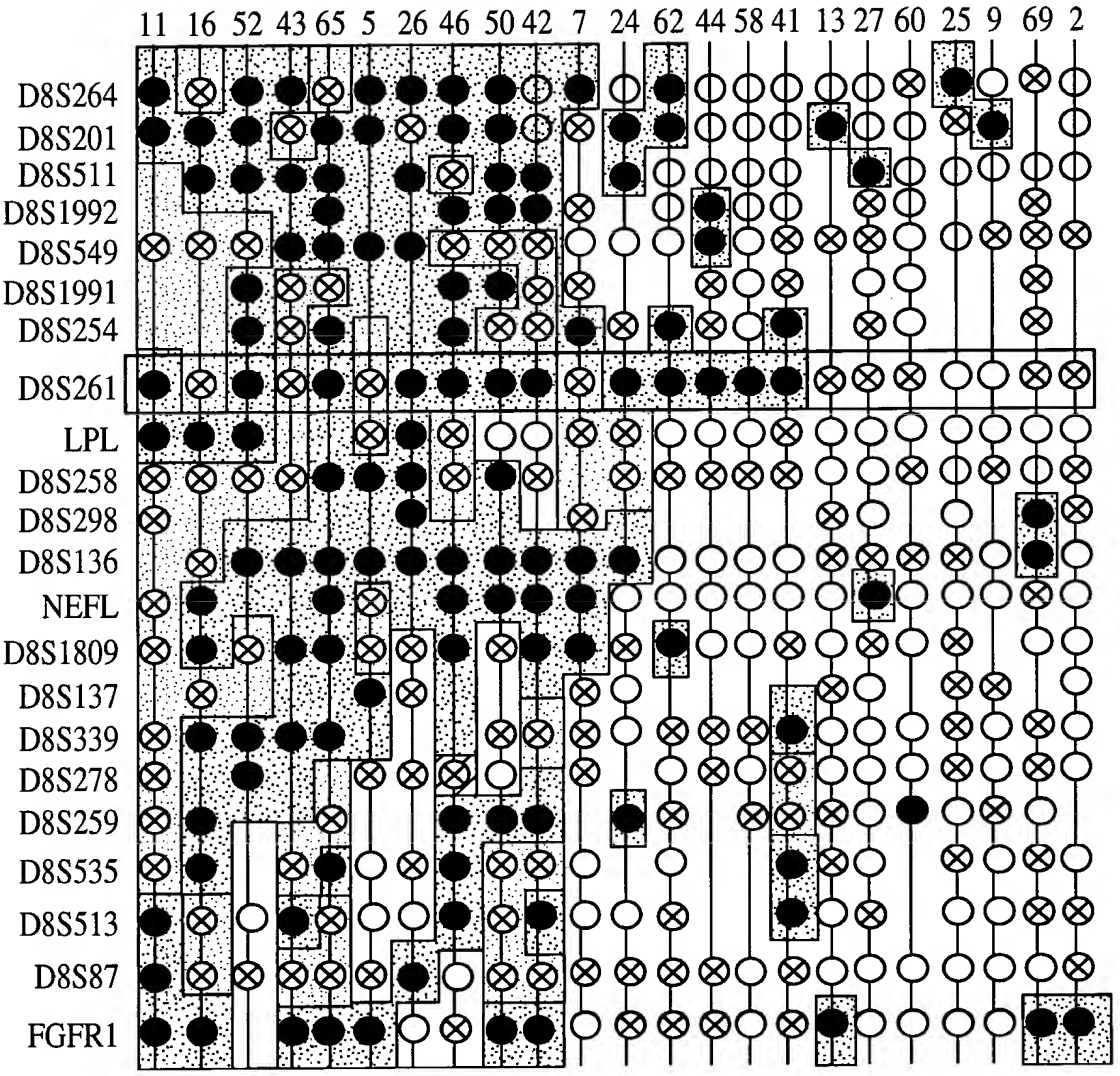
77
79
77
170
170
155
167
155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D8S511
D8S1992
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D8S261
LPL
D8S258
D8S298
D8S136
NEFL
D8S1809
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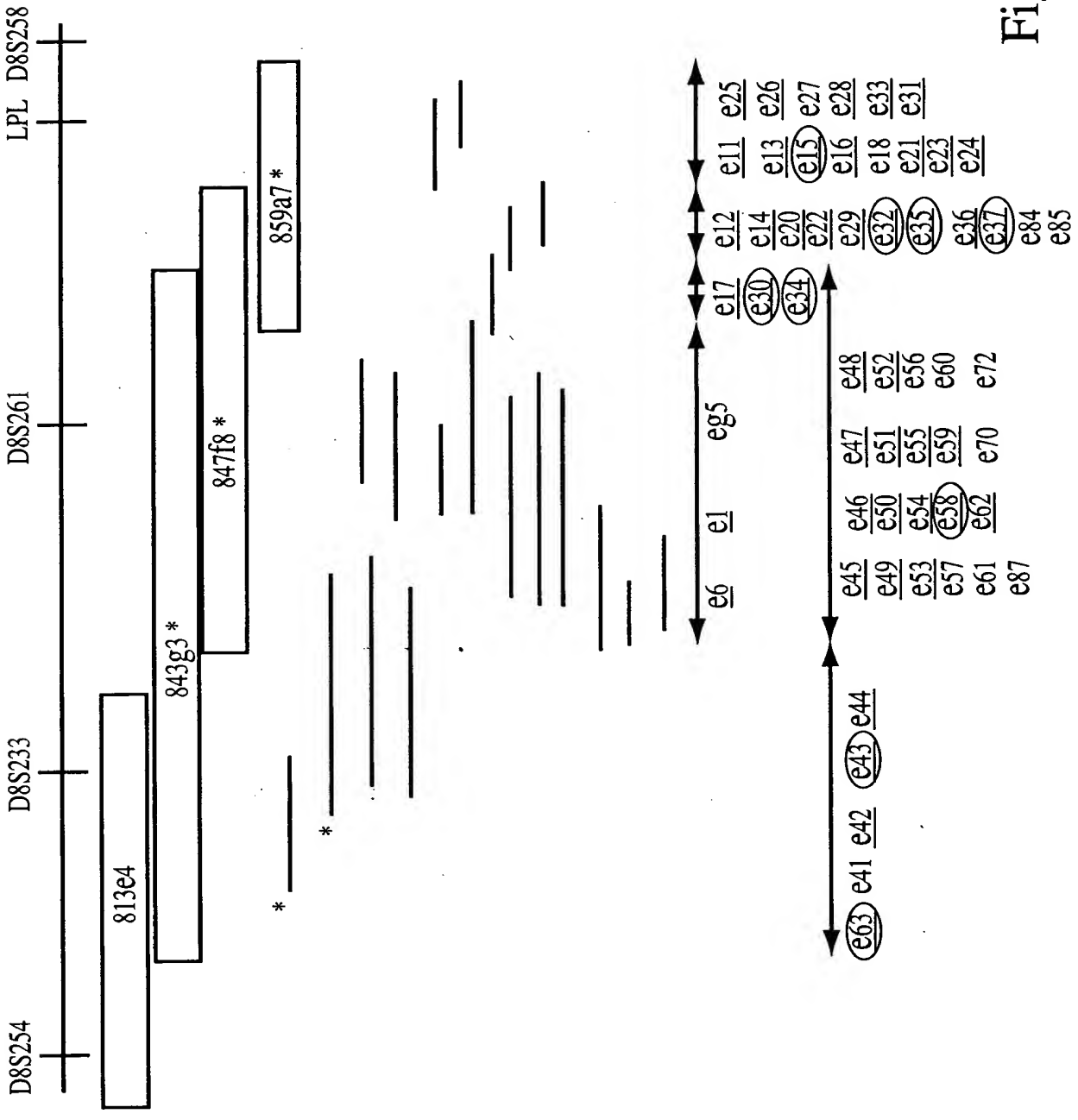
D8S259
D8S535
D8S513
D8S87
FGFR1

Fig. 1B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D8S233
D8S254
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847f8 *
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e11 e13 e15 e16 e18 e21 e23 e24
e12 e14 e20 e22 e29 e32 e35 e36 e37 e84 e85
e17 e30 e34
eg5
e1
e6
e48 e52 e56 e60 e72
e47 e51 e55 e59 e70
e46 e50 e54 e58 e62
e45 e49 e53 e57 e61 e87
e43 e44
e41 e42
e63

Fig. 1C

```
M G S V S S L I S G H S F H S K H C R A S Q Y K L R K S S H   30
L K K L N R Y S D G L L R F G F S Q D S G H G K S S S K M G   60
K S E D F F Y I K V S Q K A R G S H H P D Y T A L S S G D L   90
G G Q A G V D F D P S T P P K L M P F S N Q L E M G S E K G  120
A V R P T A F K P V L P R S G A I L H S S P E S A S H Q L H  150
P A P P D K P K E Q E L K P G L C S G A L S D S G R N S M S  180
S L P T H S T S S S Y Q L D P L V T P V G P T S R F G G S A  210
H N I T Q G I V L Q D S N M M S L K A L S F S D G G S K L G  240
H S N K A D K G P S C V R S P I S T D E C S I Q E L E Q K L  270
L E R E G A L Q K L Q R S F E E K E L A S S L A Y E E R P R  300
R C R D E L E G P E P K G G N K L K Q A S Q K S Q R A Q Q V  330
L H L Q V L Q L Q Q E K R Q L R Q E L E S L M K E Q D L L E  360
T K L R S Y E R E K T S F G P A L E E T Q W E V C Q K S G E  390
I S L L K Q Q L K E S Q T E V N A K A S E I L G L K A Q L K  420
D T R G K L E G L E L R T Q D L E G A L R T K G L E L E V C  450
E N E L Q R K K N E A E L L R E K V N L L E Q E L Q E L R A  480
Q A A L A R D M G P P T F P E D V P A L Q R E L E R L R A E  510
L R E E R Q G H D Q M S S G F Q H E R L V W K E E K E K V I  540
Q Y Q K Q L Q Q S Y V A M Y Q R N Q R L E K A L Q Q L A R G  570
D S A G E P L E V D L E G A D I P Y E D I I A T E I
```

FIG. 2A

```
KIA0522  --AWERELAELRQGCSGKLQQVARRAQRAQ--QGLQLQ
Fez1     --RCRDELEGPEPKGGNKLKQASQKSQRAQ--QVLHLQ
ATF-5    ISRRRREKENPKER--NKMAAAKCRNRRRELTDTLQAE
                                          #

KIA0522  VLRLQQDKKQLQEEAARLMRQREELEDKVAACQKE
Fez1     VLQLQQEKRQLRQELESLMKEQDLLETKLRSYERE
ATF-5    TDQLEDEKSALQTEIANLLKEKEKLEFILAAH
             #       #       #       #
```

Fig. 2B

FIG. 2C

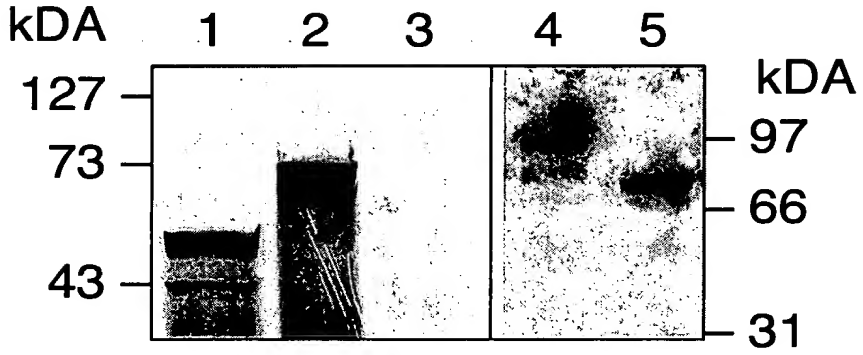
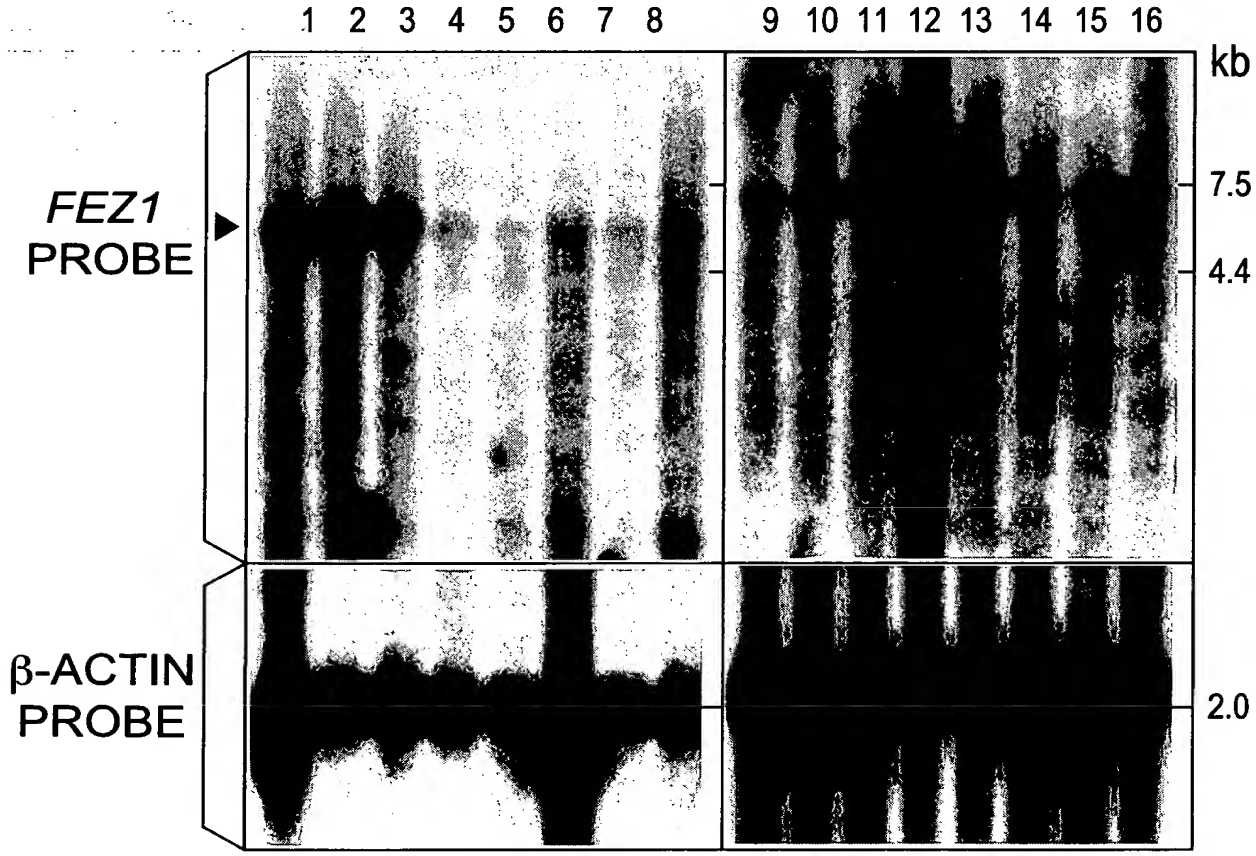

kDA
1
2
3
4
5
127
73
43
kDA
97
66
31

FIG. 2D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9 10 11 12 13 14 15 16
kb
FEZ1
PROBE
7.5
4.4
β-ACTIN
PROBE
2.0

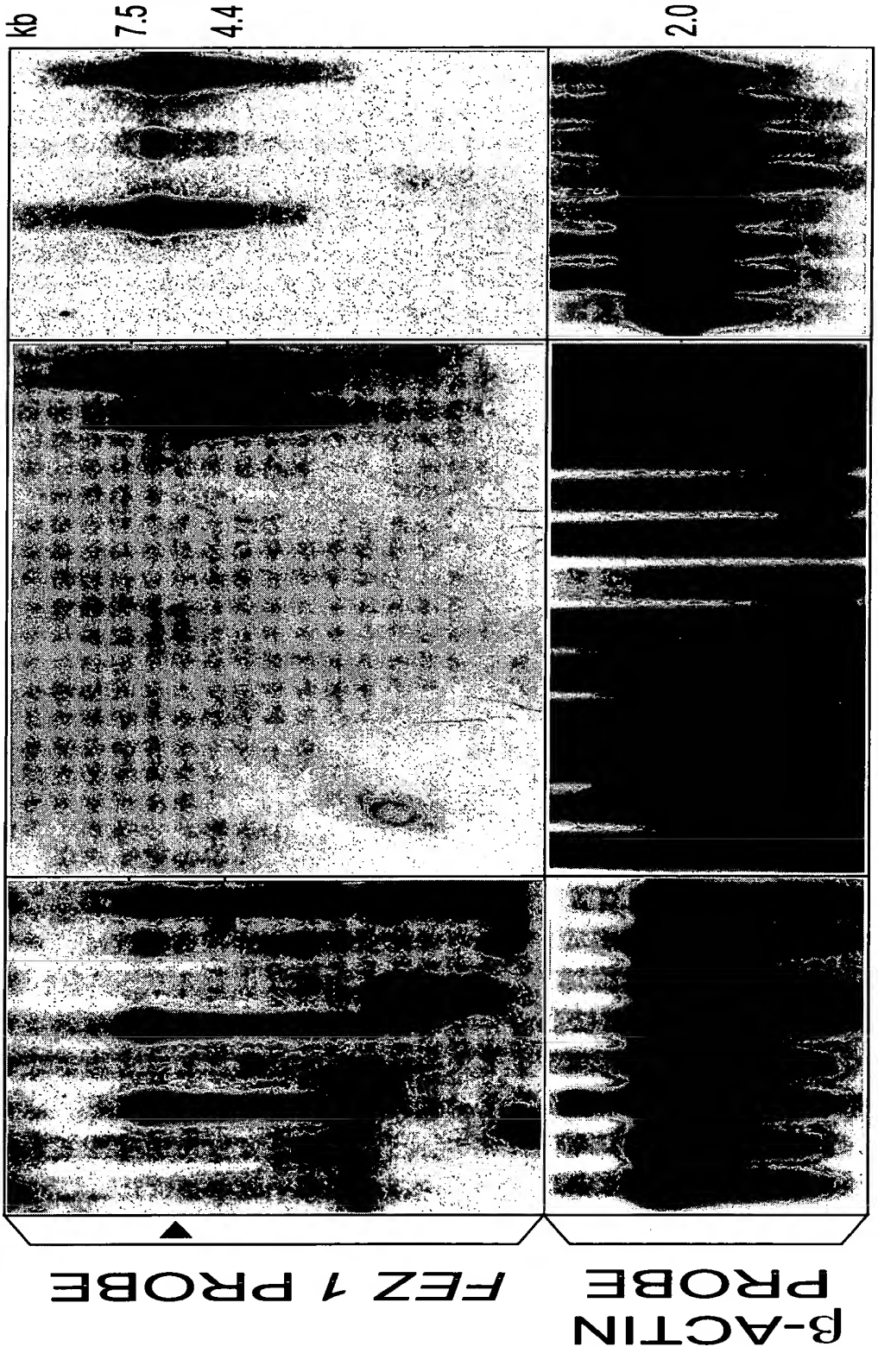
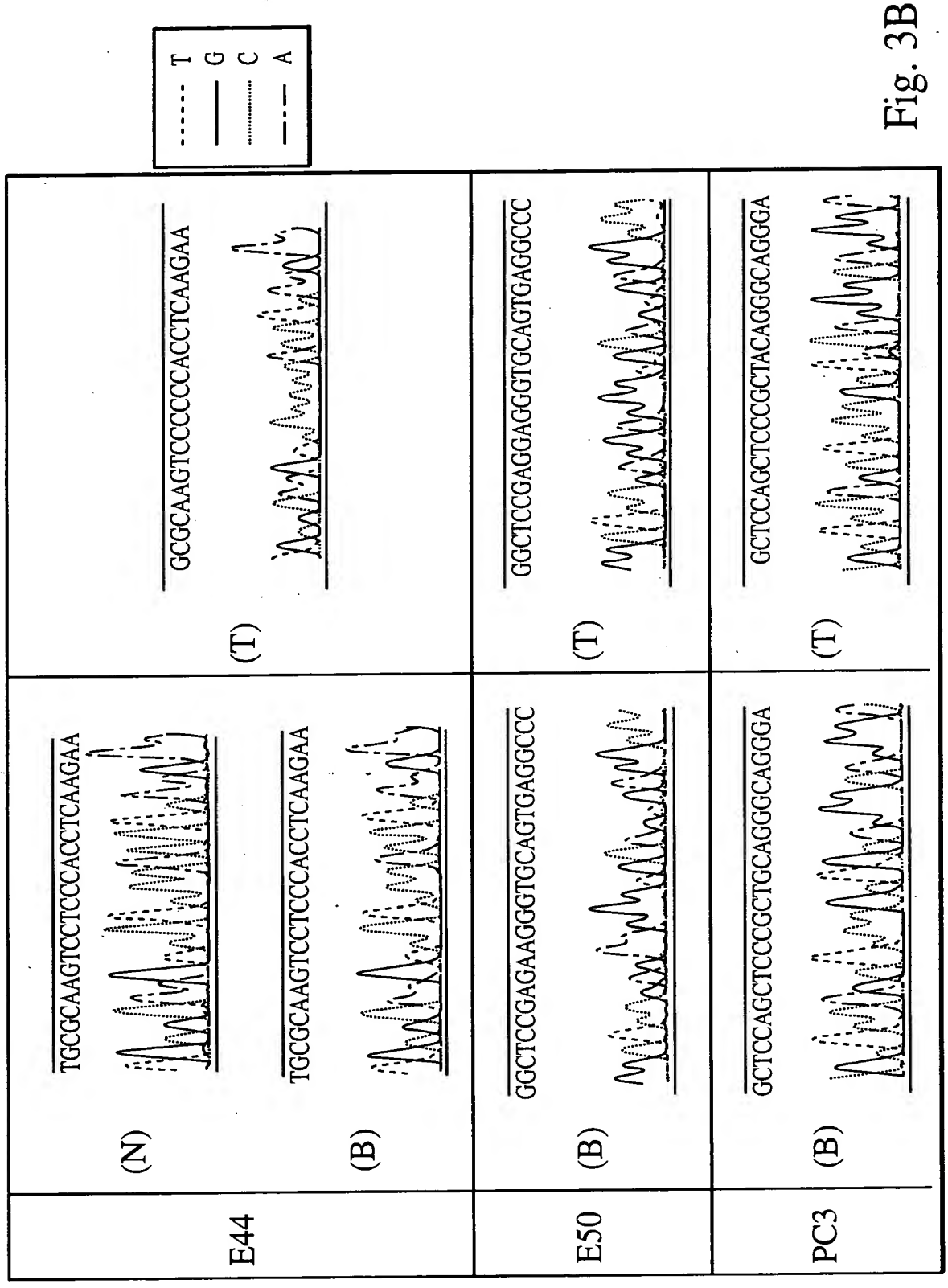

kb
7.5
4.4
2.0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28
FEZ 1 PROBE
β-ACTIN PROBE

FIG. 3A


T
G
C
A
E44
(N)
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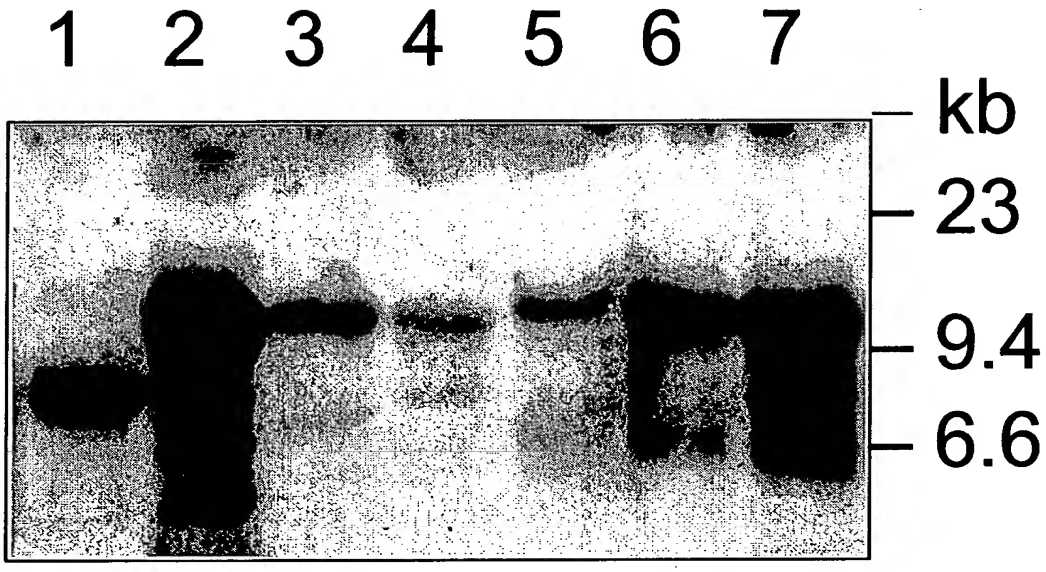
(B)
TGCGCAAGTCCTCCCACCTCAAGAA
(T)
GCGCAAGTCCCCCCACCTCAAGAA
E50
(B)
GGCTCCGAGAAGGGTGCAGTGAGGCCC
(T)
GGCTCCGAGGAGGGTGCAGTGAGGCCC
PC3
(B)
GCTCCAGCTCCCGCTGCAGGGCAGGGA
(T)
GCTCCAGCTCCCGCTACAGGGCAGGGA

Fig. 3B

FIG. 3C



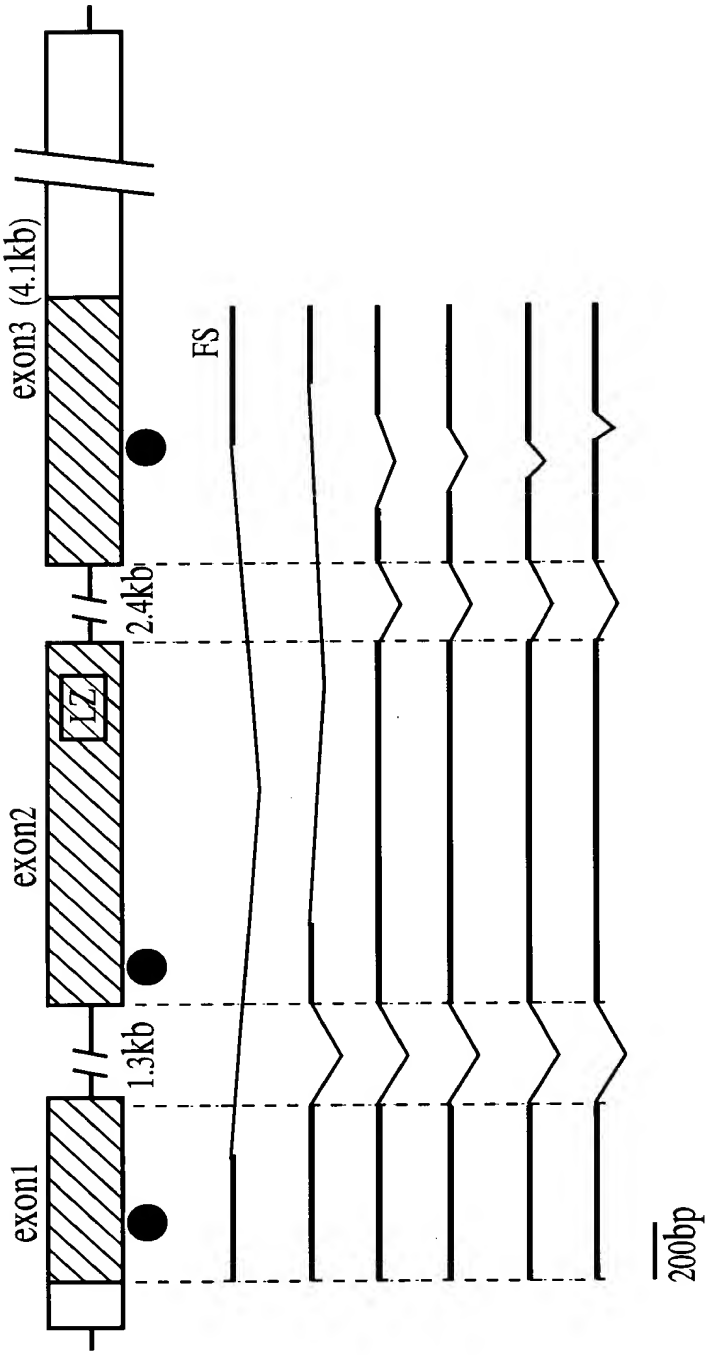
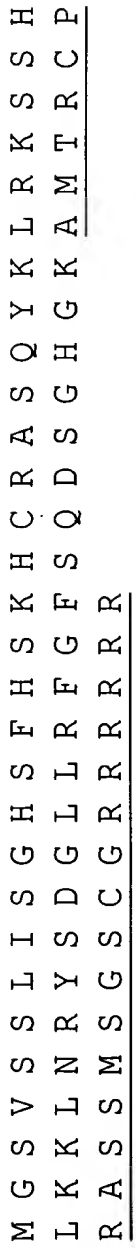


Fig. 4A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L K K L N R Y S D G L L R F G F S Q D S G H G K A M T R C P
R A S S M S G S C G R R R R R R

Fig. 4B

```
GCCTTTCCAA GACCCTGCCC GGCCCTGCCC CATCCTCAGC CCCGAGTCAC CATGGGCAGC 60
GTCAGTAGCC TCATCTCCGG CCACAGCTTC CACAGCAAGC ACTGCCGGGC TTCGCAGTAC 120
AAGCTGCGCA AGTCCTCCCA CCTCAAGAAG CTCAACCGGT ATTCCGACGG GCTGCTGAGG 180
TTTGGCTTCT CCCAGGACTC CGGTCACGGC AAGTCCAGCT CCAAAATGGG CAAGAGCGAA 240
GACTTCTTCT ACATCAAGGT CAGCCAGAAA GCCCGGGGCT CCCATCACCC AGATTACACG 300
GCACTGTCCA GCGGGGATTT AGGGGGCCAG GCTGGGGTGG ACTTTGACCC GTCCACACCC 360
CCCAAGCTCA TGCCCTTCTC CAATCAGCTA GAAATGGTAA GCGGGGGTCG CTGGCAAGGG 420
TAAGTGGGTT GGAAACGCAG GAGAAAGCAA AATGGGGGTG GAGAGCCTGG GGGTTCAGGG 480
GGAGTGGTGA CCTGAGCATT CAGACTCCTC AAAACCAGAG CGGCAGGGGT GCCGGCGGAA 540
GCCTGTGGCC ACACCGCAGA GATCAAACGT TTCACAAAGG AATTAGAGCA TCGCTCAGTC 600
CCCCTGAAGC AGAAGTCTTG GGTCAGGCCA TAAGCAAAGA GCACAGGGGA TATGTGAGCT 660
TTTGGAGTCC CACTGAAATG TAGCTGGATT GTCAACGTAG GATCCAGGCG TTTGCCAAGC 720
CTCGGGAAGG AGAGGGAGCC CTGTTCTCAT CTGGAAGCAC AGATGAAGAG GATGCAGGCC 780
GGGAGTTAAC CGCTTCTCTC CCCGGGAGAC TCGTGGGGGT GGGTGCGGTC TTCTCATTTG 840
CTGCCCTGGT GTGCATTAGC TCCTTGTTCA AGCTGCGCCT GGGGGCATCT TTGAATACAG 900
GCTGGAGTTT TGTCATCCAT TTACCAGAGA CTAGGGCAAA GGAGGCCCAG GCACTGAGAA 960
ATCCAGCCCT CACACCAGCT CAAGCCCTCG TGCGTCCCAC GAGTGGACAC TGAAATCAAT 1020
TTTCCTATTC AGTCCTCTGC CCCTTGCCCT GGGGAAATGA ATCCCCGGCT TTGATTTACT 1080
AGGAAAGAGC CTCTTATGTT TGCATAGAGC ATTCAGCTTT TCAAATTAAG GGGCTTGTAA 1140
ACTGTGAAGC ACTCTACCAG GGAAAATTAC AGTTTTAAAA AAGGATCGTG ATTTGGAGTG 1200
AGCCTCCCAA CCCTGTAAGG AGGCCAGGTC CGTGTCCTTG CTCCAGGCTT AATGGAAGAG 1260
GCAGTGAACA GGAAGAAGGG ATGGACCTAA AGAGGGACAG CAAGCTCGGC CAGCCTGATG 1320
CCCTAACTTG CCCCACACAG AGACCTAGAG CAGGAGCCTC AAGATGGTAT TTATCACCTC 1380
GGGAGGGCTG GGGCAAGCTG GTGGCAGGTT GCTATTTCAT AGAACAAAGT GCCCAAGTCG 1440
CCATTAGGGT TTTTCCCTCC TAAGAGAGAT GACATTCAGC TGCTTCAAAG CAACAGGCAA 1500
```

Fig. 5A-1

```
GGTCTGCTGA GACAATTGAC CAAGAGGGGT GCTGCGTGCG CTCAGAGAGC CCAGACTGGC 1560
TCAAGGTCGG CACGCGTGCC TGGGGAGGGA GGGTGCAATG CGCGCGCAGG GGAGGCATGA 1620
GTCACCGCGG TCCTTTTCCT CTACAGGGCT CCGAGAAGGG TGCAGTGAGG CCCACAGCCT 1680
TCAAGCCTGT GCTGCCACGG TCAGGAGCCA TCCTGCACTC CTCCCCGGAG AGTGCCAGCC 1740
ACCAGCTGCA CCCCGCCCCT CCAGACAAGC CCAAGGAGCA GGAGCTGAAG CCTGGCCTGT 1800
GCTCTGGGGC GCTGTCAGAC TCCGGCCGGA ACTCCATGTC CAGCCTGCCC ACACACAGCA 1860
CCAGCAGCAG CTACCAGCTG GACCCGCTGG TCACACCCGT GGGACCCACA AGCCGTTTTG 1920
GGGGCTCCGC CCACAACATC ACCCAGGGCA TCGTCCTCCA GGACAGCAAC ATGATGAGCC 1980
TGAAGGCTCT GTCCTTCTCC GACGGAGGTA GCAAGCTGGG CCACTCGAAC AAGGCAGACA 2040
AGGGCCCCTC GTGTGTCCGC TCCCCCATCT CCACGGACGA GTGCAGCATC CAGGAGCTGG 2100
AACAGAAGCT GTTGGAGAGG GAGGGCGCCC TCCAGAAGCT GCAGCGCAGC TTTGAGGAGA 2160
AGGAGCTTGC CTCCAGCCTG GCCTACGAGG AGCGGCCGCG GCGCTGCAGG GACGAGCTGG 2220
AGGGCCCGGA GCCCAAAGGC GGCAACAAGC TCAAGCAGGC CTCGCAGAAG AGCCAGCGCG 2280
CGCAGCAGGT CCTGCACCTG CAGGTACTGC AGCTTCAGCA GGAGAAGCGG CAGCTCCGGC 2340
AGGAGCTCGA GAGCCTCATG AAGGAGCAGG ACCTGCTGGA GACCAAGCTC AGGTCCTACG 2400
AGAGGGAGAA GACCAGCTTC GGCCCCGCGC TGGAGGAGAC CCAGTGGGAG GTGAGGCCAC 2460
ACAGGGCTCA TGGGTTTGGG TGGTCAGCGG TTTGGCGCCA GTACCCCCCT CTCCTTCTGG 2520
TGCTGGCCAA TAGCGTGCAA ACACAGACCG CGCAGGCAAG CGGGGCTAAT GTGCTGGCTT 2580
TATCACCCAA AGAAGGGGCT CCCTGCAAAC CATGTTGGGG GATCGACTTA CATCTGAGCT 2640
TCCTCCTGTC CCCACCATCA CCCTCATGGC TCCTAGATTT CAGTTTCCCA AGTGAGCCAT 2700
TAAATCATGA AGCCGGAAGC CAGATGACCA AGGCCCAGCC AGGCTGTGGG CTGACCTCCC 2760
TTCCATCAGC TCCCAGGAGG CTCAGAAGAA GAACAAGCCG TGCCTGAGTT CAGGCGGGGC 2820
CAGGGGCCCA AGAGAGCACA GAATGCATTT GTTGCTTTGG AGGGAGGGAC TGCACCCACT 2880
AGTAAGAGGG ACCCTATTGG TGGCAGGTTT CAGTGATGGA AGTGGCCACT CCTTGCTGAA 2940
GTGTAAGTGG AACTTCTATT TGGTGAGCTG AGATGGAAAC CTAGGAGAGG AAGTAAAGAG 3000
```

Fig. 5A-2

```
TCCCCCACTC ACACACTTAC ACACTCACAC ACACTCACTC ACCCGGTCAC ACGTGGAAAT 3060
GAGGCATCTG TACCTGACCG TGCTGGAGAA CCCCATAACC TCTGCATCTA TTAGTGGGAA 3120
AGCAGCTTTT CTCACCAGCC TGGTGGTCTG GATGACTCAT GGAGTTCAAG CCCATCGTTG 3180
AGGCTCTTTA CATGCTCGCA CCCAGCTTGG TCTGTCCACG TGCCTGCCTC ACCCCCAGTT 3240
CAGAGTCCAA ATCTCAGTCT ACACGCAAAC CCCTGGCTAT GTGCAAGTCA ACAACCAGTG 3300
GTTTAACTTG CCCACTGCTG GCAGCTGTAT CACCCCCATT TAACACCAAT GGTATTGGTT 3360
TTGGTGTCAG CCTGATTTCT GTCATCGATG TTTATGCCCA CATCCTCTGA CCTCACCCCT 3420
GCATGCACCC AGCCCTCCTC TCTCCTGTCT ACTGGAGTAA AGACTACCTC ACAAATTCAC 3480
TGCTGTACCC AGTGACTAGT ATCATGCTGG CTTGGATGCA GAGCCCAATC CACATCTGTC 3540
AAACGAGGAA TCATTTTCTT CTCCTCTTGC TCTTCTTTCT CTATTTCCCA CCCCTATCCC 3600
CCATCAAAAT TTGGCCAAGA GCAATGATGA AAACCGAAGC CACAGGTTAG ACCCATGTGT 3660
CTCTGGATCT TGGCCATCTG GGGTCATGGG AGACCAAGGC CAGTCTGGCT GAATCTTAAG 3720
AGTGAATGAA GTCCAGAGCA TGTGGCTCTA CAGAATGGAT TCTTGGAACT AGCCTGGAAG 3780
CCACCTTCAC ATTTCCTTTC ACAGTAGAAA TTTCCCCTTG CCCTCAGTGA AACACTGCAC 3840
AGTCCTGGAG AAAATCCGAC CCTACCCAGG ATGCGTGCTT GGGACCAAGA ATTTCATTCC 3900
AAGGCCAACC CTGTATTCAT GCCACGAAGG GAGTGACACA GTCATGGCTG AGGCATGGGC 3960
CTGGCTTTGA ACCTCAGCTT GACCACTTAT GATCCAGGTG ATTGTAAATA CATTAGCCAT 4020
GGTGGCAATG GGGTATAGTG ATTAAACTGT TGGGATCAAA TCTCTACTCT TATACTTTAT 4080
ATTTTATATA TATATATATA TAATATATAT ATATATTAGC CCTCAGGCTG GTCACTTCAC 4140
CAGCTGTTTG CTATCATAAC CTCTCTGTGC CTCAGTTTCA TTGATGTAAA TTGAGGACTA 4200
CTAATAGTAC CTACTTCATC GGGTTGTAAG GAATAGATGA GCAAATGTAT GGCTTGGCAC 4260
TTAATAACAC TACAAATTAT TAGTGAAAGT ATGTTTATAA TAATATACTT CTGTGTGGCT 4320
AGGCGTGGTG GCTCACGCCT GCAATCCCAG CACTTTGGGA GGCAGAGGCA GGCAGAGCAC 4380
TTGAGGTCAG GAATTCGAGA TCAGCCTGGC CAACATGAGG AAACCCCGTC TCTACTAAAA 4440
ATACAAAAAT CAGCCAGGCA TGGTGGCAGG TGTCTGTAAT CCCAGCTACT TGGGAGGCTG 4500
```

Fig. 5A-3

```
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CCAGCCTAGG TGACAAAGCG AGACTTCTCA AATATTAACA ATAATAATAT ACTATGTGTC 4620
ATTATACATG ATGATTATTA TTTTATCATT TTACTATATA GCCTAGCTCG ATAACCTGGG 4680
ARAAAGGTCA CAGCAATGTT CAGCTTACTT TCAGATTGGA CAAAGGCTGG AATGCCTAAC 4740
ACCGGGCCAC CGCATCCGGA GTGGCTTGGT TATTTTAGGC AGCTGAGCTG TCACTTCCCT 4800
GGGTAAGGAC ACTCACCTCT TGGCACTCTG TCTCCACCCC ACCCTCGGCA GGTGTGCCAG 4860
AAGTCAGGCG AGATCTCCCT CCTGAAGCAG CAGCTGAAGG AGTCCCAGAC GGAGGTGAAC 4920
GCCAAGGCTA GCGAGATCCT GGGTCTCAAG GCACAGCTGA AGGACACGCG GGGCAAGCTG 4980
GAGGGCCTGG AGCTGAGGAC CCAGGACCTG GAGGGCGCCC TGCGCACCAA GGGCCTGGAG 5040
CTGGAGGTCT GTGAGAATGA GCTGCAGCGC AAGAAGAACG AGGCGGAGCT GCTGCGGGAG 5100
AAGGTGAACC TGCTGGAGCA GGAGCTGCAG GAGCTGCGGG CCCAGGCCGC CCTGGCCCGC 5160
GACATGGGGC CGCCCACCTT CCCCGAGGAC GTCCCTGCCC TGCAGCGGGA GCTGGAGCGG 5220
CTGCGGGCCG AGCTGCGGGA GGAGCGGCAA GGCCATGACC AGATGTCCTC GGGCTTCCAG 5280
CATGAGCGGC TCGTGTGGAA GGAGGAGAAG GAGAAGGTGA TTCAGTACCA GAAACAGCTG 5340
CAGCAGAGCT ACGTGGCCAT GTACCAGCGG AACCAGCGCC TGGAGAAGGC CCTGCAGCAG 5400
CTGGCACGTG GGGACAGCGC CGGGGAGCCC TTGGAGGTTG ACCTGGAAGG GGCTGACATC 5460
CCCTACGAGG ACATCATAGC CACTGAGATC TGAGGGGCTG CCTGGGAAGG CGAGTCTGGG 5520
GACCTGGCAC TGGGAGGCAG GGCTCTCCCG TGCATCCCCC CTGCTCAGCA ATTCAGACCC 5580
CTCTGAGAGA CGCCACTCCC TGGGACACAG ACCCAGGACC CCCGAGGGGA GGGCAGGATG 5640
GCCTTTCCTT CCCTCTCTGA TGTCCCAGTG CTCACCAGCC CTGCAGCCCA CCAGACGTCA 5700
GGCCCTGACT CCTCTGGCTT TCCCAGGAGA TGGGTCCAGG GGTCTGTCTG CTTTGGTTAA 5760
GGGCTCCCTA AACTTTGGCC TTTGTTCGAA ATAGATATCC TCTCCCCCTC CTCCAGGGAA 5820
GGTGGCCACA GCAAGAACAG CGGCTCCCCT CCGCTTCTCA TCCCAACCTC TTTTTCCTCC 5880
TGGACACATT GGAATGCCTT GGAAATAGAA AGAAGCCATA TATGACCAGA AGCCTTGGAA 5940
CCAGCCCCAT CAGAACCTGA GCTATTTTCC TCTGGCCGCA GAGGTGTAGG GGTGGAATGA 6000
```

Fig. 5A-4

```
GCCGCGGGGA AGCTGGCTTT GAAACCTCAG GGCTGTCCCA GCCCCGGCAA GCCACAGGAA 6060
GGAGGGGAGA GACAGGCAGC CCAGCAGTGT GGAGACCCTG CCACAGCCAG AGGAGGGCAG 6120
AGGGAGAATC CAAGGGTTGA GAGCCAGTGG CGGGTGATGG CCAGCCCCTG GGGCCCAGCC 6180
CCTGTTTACT GGTTCTTGCA AATGGGAGCT GAGCAGCCTC TGGACAGCCA GTGACCTTTG 6240
ACCTCGGTGA CCACTCTTCT TTAAGCCATA GACCCTGAGG CCCTGGGCTG GGTGCTGGGA 6300
AGGGAGGGTT GAAACCACCG TGAACCAGAG GGTGTGGCTT TCCAGKCACC CTCAGGGAGC 6360
CTCCCCATCT GTCCAGCTGG GGCCAGAGGC TGGGAGTCCC TACCTGCTTC ACGTTGGCCG 6420
GCGGCTACTC TGGAATGTTT TTCCCTCCCC AGAATCAAGC TTTTGCTTGA TCCAGAAGAG 6480
CCCATATCAC TAAGATGGCA TATATGTGAT CTGGGCATTT TCCTCCTCTG CCTACAGCCA 6540
GGTTTAGCGG CAAACCTTTC CCCCTTAGCA CCTTCAGGGC TGAGTTCTGG GTTTCTAGAG 6600
GTCAGGACGG CTCCTCAGAG CGCCAGGAAG CCAGAGCCCC AAGCAGGACG AAAAAGAGGC 6660
ATACACACAG CAGTGTGAAT AGCCTGGCCA CCAGCCATCC TCCCTCCACC TCAAGACCCC 6720
CATTTGTCCS AGACTAAAGG ATCCAGAGAG CAGCTCCCTT TCTCAGGAGC TTGGGCAGTG 6780
CCCCAGGGAG TCCAGGGTTT CTCTGCAGAT GTGCGGAGCG GGAGGCGGTG GTAGAGAGAG 6840
ATAAAAGGTG GAGTTTCTCT GTTGTTTGGT TCAGGGATTT TATTTTTAAT TTTATGAGAC 6900
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TCATACTCCT GGGCTCAAGC AATCCTCCTG CCTCAGCCTT CCAACTAGCT GGGACTACAG 7020
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GTTGCCAAAG CTGGTCTCAA ACTTGTGGCC TCAAGCAATC CACCTGCCTT GGCCTCCCAA 7140
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GCCAGTCCCC ATTTCTGCCT CGCTCACCGC TGGCCCTTAG AGACCCCGAG GTAGGGGTGG 7440
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```

Fig. 5A-5

```
CTGAGGCCAG AGTCACCTTT TCTGTGGCTG GCTCTACCTT CCTGTCCCTG AGGTTAAACG 7560
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CTTAGTCCCA AGCTAGGCTT AAACCTGGAA TCTACAAGCC AAAAGTCCCT CCCTGCCTGA 7680
GGGCAGTACC CTCCATTGGG CACAGTCCAG ACCCAAGTCA AAGATGCCCC ATTCCTTGCG 7740
CCTCAGCCCT CAGTTCCTTC ATTTCCACCA GGCCGTGCCT TGTTTGAGTT TTTCCTCCCA 7800
GTGAGACTGC CCCACGGAGA CAGAGGAAAG GGCTGGCTCC CCCTCCCCAG GCTGGAGACC 7860
CCCCCCAACT CCAGGAAAGA GCAGTCAGAG TCCAGTGCTC TGCCTCAGAC GTTGCCTGAG 7920
AAGAAGTGGC TGCCACACCC AGGGGAAGGC CCTGAGGCGG AGGCTGTGCT CCGCCATGGT 7980
GTCCCGGTAC CTTCCATACA CAGAGGAGTG CAGCCTTCTC CATATCTCCA TGGCCCTGTC 8040
CCAGGCCGGC CCAGATGTGT CCCCCCCAGG CCTTGTCCTA CGTCCAAGGT GGCAGATGTC 8100
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CGCCCTCACT ATTCTTGGAC CATGCCAGAT TCTGCCTCTC TGGAAAGAGG CTCTGGACAG 8280
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TCCCTCTGGG CACGCCTGCT GGCCGACCCA CTGACCCACT CGGATGGACC AACCTGCTCT 8400
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CTCTGCCCCT GGACCTGGGA ACGACTGGAC TGTCACGGGG TTCCCTCCTA GCTCTCCCAG 8520
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CAGAGGCTGC ACCCCTGGGC CAGCGGGGCT GCTCACCCAC CTCTTGTGCA AGGTGGCCTT 8820
TGTGCTGCGC CTGCAGGCAG AGCTGGAGCC CCCAGCAGAG GCAGGCTGGG ACGGACCAGC 8880
ATCTGGAAGA TGTACATAGT TATTTTTCTC TTTGTGGTTT CTTGTTTGGT TTGGTTTGCT 8940
TTTGACAGCT TCATTTTATT TTTGACGTCA CTTTTTGGCC ATGTAAACTA TTTGTGGCAA 9000
TTTTATGTTT TTATTTATGA ATAAAGAATG CCATTTCTCA CGCCCTCT              9048
```

Fig. 5A-6

```
TGAGGGCTTT GCTATGACCT CAGTCCCCTC ACGGAGCCAC GACTGCCCCT TGCTGCCACA 60
GCCTTTCCAA GACCCTGCCC GGCCCTGCCC CATCCTCAGC CCCGAGTCAC CATGGGCAGC 120
GTCAGTAGCC TCATCTCCGG CCACAGCTTC CACAGCAAGC ACTGCCGGGC TTCGCAGTAC 180
AAGCTGCGCA AGTCCTCCCA CCTCAAGAAG CTCAACCGGT ATTCCGACGG GCTGCTGAGG 240
TTTGGCTTCT CCCAGGACTC CGGTCACGGC AAGTCCAGCT CCAAAATGGG CAAGAGCGAA 300
GACTTCTTCT ACATCAAGGT CAGCCAGAAA GCCCGGGGCT CCCATCACCC AGATTACACG 360
GCACTGTCCA GCGGGGATTT AGGGGGCCAG GCTGGGGTGG ACTTTGACCC GTCCACACCC 420
CCCAAGCTCA TGCCCTTCTC CAATCAGCTA GAAATGGGCT CCGAGAAGGG TGCAGTGAGG 480
CCCACAGCCT TCAAGCCTGT GCTGCCACGG TCAGGAGCCA TCCTGCACTC CTCCCCGGAG 540
AGTGCCAGCC ACCAGCTGCA CCCCGCCCCT CCAGACAAGC CCAAGGAGCA GGAGCTGAAG 600
CCTGGCCTGT GCTCTGGGGC GCTGTCAGAC TCCGGCCGGA ACTCCATGTC CAGCCTGCCC 660
ACACACAGCA CCAGCAGCAG CTACCAGCTG GACCCGCTGG TCACACCCGT GGGACCCACA 720
AGCCGTTTTG GGGGCTCCGC CCACAACATC ACCCAGGGCA TCGTCCTCCA GGACAGCAAC 780
ATGATGAGCC TGAAGGCTCT GTCCTTCTCC GACGGAGGTA GCAAGCTGGG CCACTCGAAC 840
AAGGCAGACA AGGGCCCCTC GTGTGTCCGC TCCCCCATCT CCACGGACGA GTGCAGCATC 900
CAGGAGCTGG AGCAGAAGCT GTTGGAGAGG GAGGGCGCCC TCCAGAAGCT GCAGCGCAGC 960
TTTGAGGAGA AGGAGCTTGC CTCCAGCCTG GCCTACGAGG AGCGGCCGCG GCGCTGCAGG 1020
GACGAGCTGG AGGGCCCGGA GCCCAAAGGC GGCAACAAGC TCAAGCAGGC CTCGCAGAAG 1080
AGCCAGCGCG CGCAGCAGGT CCTGCACCTG CAGGTACTGC AGCTTCAGCA GGAGAAGCGG 1140
CAGCTCCGGC AGGAGCTCGA GAGCCTCATG AAGGAGCAGG ACCTGCTGGA GACCAAGCTC 1200
AGGTCCTACG AGAGGGAGAA GACCAGCTTC GGCCCCGCGC TGGAGGAGAC CCAGTGGGAG 1260
GTGTGCCAGA AGTCAGGCGA GATCTCCCTC CTGAAGCAGC AGCTGAAGGA GTCCCAGACG 1320
GAGGTGAACG CCAAGGCTAG CGAGATCCTG GGTCTCAAGG CACAGCTGAA GGACACGCGG 1380
GGCAAGCTGG AGGGCCTGGA GCTGAGGACC CAGGACCTGG AGGGCGCCCT GCGCACCAAG 1440
GGCCTGGAGC TGGAGGTCTG TGAGAATGAG CTGCAGCGCA AGAAGAACGA GGCGGAGCTG 1500
```

Fig. 5B-1

```
CTGCGGGAGA AGGTGAACCT GCTGGAGCAG GAGCTGCAGG AGCTGCGGGC CCAGGCCGCC 1560
CTGGCCCGCG ACATGGGGCC GCCCACCTTC CCCGAGGACG TCCCTGCCCT GCAGCGGGAG 1620
CTGGAGCGGC TGCGGGCCGA GCTGCGGGAG GAGCGGCAAG GCCATGACCA GATGTCCTCG 1680
GGCTTCCAGC ATGAGCGGCT CGTGTGGAAG GAGGAGAAGG AGAAGGTGAT TCAGTACCAG 1740
AAACAGCTGC AGCAGAGCTA CGTGGCCATG TACCAGCGGA ACCAGCGCCT GGAGAAGGCC 1800
CTGCAGCAGC TGGCACGTGG GGACAGCGCC GGGGAGCCCT TGGAGGTTGA CCTGGAAGGG 1860
GCTGACATCC CCTACGAGGA CATCATAGCC ACTGAGATCT GAGGGGCTGC CTGGGAAGGC 1920
GAGTCTGGGG ACCTGGCACT GGGAGGCAGG GCTCTCCCGT GCATCCCCCC TGCTCAGCAA 1980
TTCAGACCCC TCTGAGAGAC GCCACTCCCT GGGACACAGA CCCAGGACCC CCGAGGGGAG 2040
GGCAGGATGG CCTTTCCTTC CCTCTCTGAT GTCCCAGTGC TCACCAGCCC TGCAGCCCAC 2100
CAGACGTCAG GCCCTGACTC CTCTGGCTTT CCCAGGAGAT GGGTCCAGGG GTCTGTCTGC 2160
TTTGGTTAAG GGCTCCCTAA ACTTTGGCCT TTGTTCGAAA TAGATATCCT CTCCCCCTCC 2220
TCCAGGGAAG GTGGCCACAG CAAGAACAGC GGCTCCCCTC CGCTTCTCAT CCCAACCTCT 2280
TTTTCCTCCT GGACACATTG GAATGCCTTG GAAATAGAAA GAAGCCATAT ATGACCAGAA 2340
GCCTTGGAAC CAGCCCCATC AGAACCTGAG CTATTTTCCT CTGGCCGCAG AGGTGTAGGG 2400
GTGGAATGAG CCGCGGGGAA GCTGGCTTTG AAACCTCAGG GCTGTCCCAG CCCCGGCAAG 2460
CCACAGGAAG GAGGGGAGAG ACAGGCAGCC CAGCAGTGTG GAGACCCTGC CACAGCCAGA 2520
GGAGGGCAGA GGGAGAATCC AAGGGTTGAG AGCCAGTGGC GGGTGATGGC CAGCCCCTGG 2580
GGCCCAGCCC CTGTTTACTG GTTCTTGCAA ATGGGAGCTG AGCAGCCTCT GGACAGCCAG 2640
TGACCTTTGA CCTCGGTGAC CACTCTTCTT TAAGCCATAG ACCCTGAGGC CCTGGGCTGG 2700
GTGCTGGGAA GGGAGGGTTG AAACCACCGT GAACCAGAGG GTGTGGCTTT CCAGGCACCC 2760
TCAGGGAGCC TCCCCATCTG TCCAGCTGGG GCCAGAGGCT GGGAGTCCCT ACCTGCTTCA 2820
CGTTGGCCGG CGGCTACTCT GGAATGTTTT TCCCTCCCCA GAATCAAGCT TTTGCTTGAT 2880
CCAGAAGAGC CCATATCACT AAGATGGCAT ATATGTGATC TGGGCATTTT CCTCCTCTGC 2940
CTACAGCCAG GTTTAGCGGC AAACCTTTCC CCCTTAGCAC CTTCAGGGCT GAGTTCTGGG 3000
```

Fig. 5B-2

```
TTTCTAGAGG TCAGGACGGC TCCTCAGAGC GCCAGGAAGC CAGAGCCCCA AGCAGGACGA 3060
AAAAGAGGCA TACACACAGC AGTGTGAATA GCCTGGCCAC CAGCCATCCT CCCTCCACCT 3120
CAAGACCCCC ATTTGTCCCA GACTAAAGGA TCCAGAGAGC AGCTCCCTTT CTCAGGAGCT 3180
TGGGCAGTGC CCCAGGGAGT CCAGGGTTTC TCTGCAGATG TGCGGAGCGG GAGGCGGTGG 3240
TAGAGAGAGA TAAAAGGTGG AGTTTCTCTG TTGTTTGGTT CAGGGATTTT ATTTTTAATT 3300
TTATGAGACA GGGTCTTGCT CTGTCCCCCA GGCTGGAGTG CAGTGGCATG ATCATAGCTC 3360
ACTGCAGCCT CATACTCCTG GGCTCAAGCA ATCCTCCTGC CTCAGCCTTC CAACTAGCTG 3420
GGACTACAGG TGCGCGCCAC CGTGCCTGGC TAACTTTTCA TTTTTTTTGT AGGGACGGGG 3480
TCTCGTTTTG TTGCCAAAGC TGGTCTCAAA CTTGTGGCCT CAAGCAATCC ACCTGCCTTG 3540
GCCTCCCAAA GTGCTGAGAT TGCAGATGTG AGCCACCGTG CCTGGCCAGA TTTTTCTTTT 3600
ATTCTTCTTT CTTTTTCTTT TTTGCTTTCT TGTCTTTTCA GAAGCAAGCC AGACCTAGCA 3660
GGCTGTTCCA TGTTCTATTT TTGACTGTAG CCACAGCTGC TGTTCTCAGG ACAGCATCCC 3720
TTCCCACATG CCTGCGCCTG CTGCCTGCTG AGATGAGGAG GGGAGCGTCT GGGAACTTGC 3780
GAGTCCAAGG CCAGTCCCCA TTTCTGCCTC GCTCACCGCT GGCCCTTAGA GACCCCGAGG 3840
TAGGGGTGGG GAGATGCTTC TCTCCTTGCC CCCCGCCCTC ATGGGTCCTA GCCCTTCCCT 3900
GAGTGCGGGC TGAGGCCAGA GTCACCTTTT CTGTGGCTGG CTCTACCTTC CTGTCCCTGA 3960
GGTTAAACGG TGCCCATCCT GCCATCCTCA AACGACAGAG GAGCTTTTCT GGAATTTCAA 4020
ACCATTGCTC TTAGTCCCAA GCTAGGCTTA AACCTGGAAT CTACAAGCCA AAAGTCCCTC 4080
CCTGCCTGAG GGCAGTACCC TCCATTGGGC ACAGTCCAGA CCCAAGTCAA AGATGCCCCA 4140
TTCCTTGCGC CTCAGCCCTC AGTTCCTTCA TTTCCACCAG GCCGTGCCTT GTTTGAGTTT 4200
TTCCTCCCAG TGAGACTGCC CCACGGAGAC AGAGGAAAGG GCTGGCTCCC CCTCCCCAGG 4260
CTGGAGACCC CCCCCAACTC CAGGAAAGAG CAGTCAGAGT CCAGTGCTCT GCCTCAGACG 4320
TTGCCTGAGA AGAAGTGGCT GCCACACCCA GGGGAAGGCC CTGAGGCGGA GGCTGTGCTC 4380
CGCCATGGTG TCCCGGTACC TTCCATACAC AGAGGAGTGC AGCCTTCTCC ATATCTCCAT 4440
GGCCCTGTCC CAGGCCGGCC CAGATGTGTC CCCCCCAGGC CTTGTCCTAC GTCCAAGGTG 4500
```

Fig. 5B-3

```
GCAGATGTCT TCCCTGGGCT GCCACCAGCC CCCGCCCCAG AGTGGCCCAC CGTGGCACTA 4560
GAATGCAAGT ATCCTGCGAC CTTGCAACCT CACCTTCCTG TGGGTGTTCT TTCCTGCCCT 4620
GTCCAAAAGC GCCCTCACTA TTCTTGGACC ATGCCAGATT CTGCCTCTCT GGAAAGAGGC 4680
TCTGGACAGC AGAAGCCTCC AAGCACAGAG CCTGGCCCCA GGCCCCAGAC AGGGTGGGCT 4740
TCCTGCCCTT CCCTCTGGGC ACGCCTGCTG GCCGACCCAC TGACCCACTC GGATGGACCA 4800
ACCTGCTCTG TCCCCAAAGG ACGCCTGCAG GAGAGAGCAG CACTCCGCAT CACCTCACCA 4860
AGGATCGGAC TCTGCCCCTG GACCTGGGAA CGACTGGACT GTCACGGGGT TCCCTCCTAG 4920
CTCTCCCAGT GAACTCCTGC CAGGCACACA CAGCCCCTAT AGCACTGAGC TCACATGGGA 4980
CTGGGATATG GGGGCATCTC TTCCCCAGAG AGGCACTCAG TGAGCCTCCT GTGCCTGGCC 5040
CCAGTCTGGG CCATCTCTTA GGTGAGACAG TTGCCCGAAA CTAAGCCAGG CCTGGCTGGA 5100
GGAGCAGCAG CTTGGGGAGA GGGATTTCCC TGCAGACCTC AAGCCATCAT GCGGTGGGTG 5160
CTGCCATGAC AGAGGCTGCA CCCCTGGGCC AGCGGGGCTG CTCACCCACC TCTTGTGCAA 5220
GGTGGCCTTT GTGCTGCGCC TGCAGGCAGA GCTGGAGCCC CCAGCAGAGG CAGGCTGGGA 5280
CGGACCAGCA TCTGGAAGAT GTACATAGTT ATTTTTCTCT TTGTGGTTTC TTGTTTGGTT 5340
TGGTTTGCTT TTGACAGCTT CATTTTATTT TTGACGTCAC TTTTTGGCCA TGTAAACTAT 5400
TTGTGGCAAT TTTATGTTTT TATTTATGAA TAAAGAATGC CATTTCTCAC GCCCTCTAAA 5460
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                               5492
```

Fig. 5B-4

```
ATGGGCAGCG TCAGTAGCCT CATCTCCGGC CACAGCTTCC ACAGCAAGCA CTGCCGGGCT 60
TCGCAGTACA AGCTGCGCAA GTCCTCCCAC CTCAAGAAGC TCAACCGGTA TTCCGACGGG 120
CTGCTGAGGT TTGGCTTCTC CCAGGACTCC GGTCACGGCA AGGCCATGAC CAGATGTCCT 180
CGGGCTTCCA GCATGAGCGG CTCGTGTGGA AGGAGGAGAA GGAGAAGGTG ATTCAGTACC 240
AGAAACAGCT GCAGCAGAGC TACGTGGCCA TGTACCAGCG GAACCAGCGC CTGGAGAAGG 300
CCCTGCAGCA GCTGGCACGT GGGGACAGCG CCGGGGAGCC CTTGGAGGTT GACCTGGAAG 360
GGGCTGACAT CCCCTACGAG GACATCATAG CCACTGAGAT CTGA                 404
```

Fig. 5C

```
ATGGGCAGCG TCAGTAGCCT CATCTCCGGC CACAGCTTCC ACAGCAAGCA CTGCCGGGCT 60
TCGCAGTACA AGCTGCGCAA GTCCTCCCAC CTCAAGAAGC TCAACCGGTA TTCCGACGGG 120
CTGCTGAGGT TTGGCTTCTC CCAGGACTCC GGTCACGGCA AGTCCAGCTC CAAAATGGGC 180
AAGAGCGAAG ACTTCTTCTA CATCAAGGTC AGCCAGAAAG CCCGGGGCTC CCATCACCCA 240
GATTACACGG CACTGTCCAG CGGGGATTTA GGGGGCCAGG CTGGGGTGGA CTTTGACCCG 300
TCCACACCCC CCAAGCTCAT GCCCTTCTCC AATCAGCTAG AAATGGGCTC CGAGAAGGGT 360
GCAGTGAGGC CCACAGCCTT CAAGCCTGTG CTGCCACGGT CAGGAGCCAT CCTGCACTCC 420
TCCCCGGAGA GTGCCAGCCA CCAGCTGCAC CCCGCCCCTC CAGACAAGCC CAAGGAGCAG 480
GAGCTGAAGC CTGGCCTGTG CTCTGGGGCG CTGTCAGACT CCGGCCGGAA CTCCATGTCC 540
AGCCTGCCCA CACACAGCGC CGGGGAGCCC TTGGAGGTTG ACCTGGAAGG GGCTGACATC 600
CCCTACGAGG ACATCATAGC CACTGAGATC TGA                             633
```

Fig. 5D

```
ATGGGCAGCG TCAGTAGCCT CATCTCCGGC CACAGCTTCC ACAGCAAGCA CTGCCGGGCT 60
TCGCAGTACA AGCTGCGCAA GTCCTCCCAC CTCAAGAAGC TCAACCGGTA TTCCGACGGG 120
CTGCTGAGGT TTGGCTTCTC CCAGGACTCC GGTCACGGCA AGTCCAGCTC CAAAATGGGC 180
AAGAGCGAAG ACTTCTTCTA CATCAAGGTC AGCCAGAAAG CCCGGGGCTC CCATCACCCA 240
GATTACACGG CACTGTCCAG CGGGGATTTA GGGGGCCAGG CTGGGGTGGA CTTTGACCCG 300
TCCACACCCC CCAAGCTCAT GCCCTTCTCC AATCAGCTAG AAATGGGCTC CGAGAAGGGT 360
GCAGTGAGGC CCACAGCCTT CAAGCCTGTG CTGCCACGGT CAGGAGCCAT CCTGCACTCC 420
TCCCCGGAGA GTGCCAGCCA CCAGCTGCAC CCCGCCCCTC CAGACAAGCC CAAGGAGCAG 480
GAGCTGAAGC CTGGCCTGTG CTCTGGGGCG CTGTCAGACT CCGGCCGGAA CTCCATGTCC 540
AGCCTGCCCA CACACAGCAC CAGCAGCAGC TACCAGCTGG ACCCGCTGGT CACACCCGTG 600
GGACCCACAA GCCGTTTTGG GGGCTCCGCC CACAACATCA CCCAGGGCAT CGTCCTCCAG 660
GACAGCAACA TGATGAGCCT GAAGGCTCTG TCCTTCTCCG ACGGAGGTAG CAAGCTGGGC 720
CACTCGAACA AGGCAGACAA GGGCCCCTCG TGTGTCCGCT CCCCCATCTC CACGGACGAG 780
TGCAGCATCC AGGAGCTGGA GCAGAAGCTG TTGGAGAGGG AGGGCGCCCT CCAGAAGCTG 840
CAGCGCAGCT TTGAGGAGAA GGAGCTTGCC TCCAGCCTGG CCTACGAGGA GCGGCCGCGG 900
CGCTGCAGGG ACGAGCTGGA GGGCCCGGAG CCCAAAGGCG GCAACAAGCT CAAGCAGGCC 960
TCGCAGAAGA GCCAGCGCGC GCAGCAGGTC CTGCACCTGC AGGTACTGCA GCTTCAGCAG 1020
GAGAAGCGGC AGCTCCGGCA GGAGCTCGAG AGCCTCATGA AGGAGCAGGA CCTGCTGGAG 1080
ACCAAGCTCA GGTCCTACGA GAGGGAGAAG ACCAGCTTCG GCCCCGCGCT GGAGGAGACC 1140
CAGTGGGAGG TGTGCCAGAA GTCAGGCGAG ATCTCCCTCC TGAAGCAGCA GCTGAAGGAG 1200
TCCCAGACGG AGGTGAACGC CAAGGCTAGC GAGATCCTGG GTCTCAAGGC ACAGCTGAAG 1260
GACACGCGGG GCAAGCTGGA GGGCCTGGAG CTGAGGACCC AGGACCTGGA GGGCGCCCTG 1320
CGCACCAAGG GCCTGGAGCT GGAGGTCTGT GAGAATGAGC TGCAGCGCAA GAAGAACGAG 1380
GCGGAGCTGC TGCGGGAGAA GCATGAGCGG CTCGTGTGGA AGGAGGAGAA GGAGAAGGTG 1440
```

Fig. 5E-1

```
ATTCAGTACC AGAAACAGCT GCAGCAGAGC TACGTGGCCA TGTACCAGCG GAACCAGCGC 1500
CTGGAGAAGG CCCTGCAGCA GCTGGCACGT GGGGACAGCG CCGGGGAGCC CTTGGAGGTT 1560
GACCTGGAAG GGGCTGACAT CCCCTACGAG GACATCATAG CCACTGAGAT CTGA
1614
```

Fig. 5E-2

```
ATGGGCAGCG TCAGTAGCCT CATCTCCGGC CACAGCTTCC ACAGCAAGCA CTGCCGGGCT 60
TCGCAGTACA AGCTGCGCAA GTCCTCCCAC CTCAAGAAGC TCAACCGGTA TTCCGACGGG 120
CTGCTGAGGT TTGGCTTCTC CCAGGACTCC GGTCACGGCA AGTCCAGCTC CAAAATGGGC 180
AAGAGCGAAG ACTTCTTCTA CATCAAGGTC AGCCAGAAAG CCCGGGGCTC CCATCACCCA 240
GATTACACGG CACTGTCCAG CGGGGATTTA GGGGGCCAGG CTGGGGTGGA CTTTGACCCG 300
TCCACACCCC CCAAGCTCAT GCCCTTCTCC AATCAGCTAG AAATGGGCTC CGAGAAGGGT 360
GCAGTGAGGC CCACAGCCTT CAAGCCTGTG CTGCCACGGT CAGGAGCCAT CCTGCACTCC 420
TCCCCGGAGA GTGCCAGCCA CCAGCTGCAC CCCGCCCCTC CAGACAAGCC CAAGGAGCAG 480
GAGCTGAAGC CTGGCCTGTG CTCTGGGGCG CTGTCAGACT CCGGCCGGAA CTCCATGTCC 540
AGCCTGCCCA CACACAGCAC CAGCAGCAGC TACCAGCTGG ACCCGCTGGT CACACCCGTG 600
GGACCCACAA GCCGTTTTGG GGGCTCCGCC CACAACATCA CCCAGGGCAT CGTCCTCCAG 660
GACAGCAACA TGATGAGCCT GAAGGCTCTG TCCTTCTCCG ACGGAGGTAG CAAGCTGGGC 720
CACTCGAACA AGGCAGACAA GGGCCCCTCG TGTGTCCGCT CCCCCATCTC CACGGACGAG 780
TGCAGCATCC AGGAGCTGGA GCAGAAGCTG TTGGAGAGGG AGGGCGCCCT CCAGAAGCTG 840
CAGCGCAGCT TTGAGGAGAA GGAGCTTGCC TCCAGCCTGG CCTACGAGGA GCGGCCGCGG 900
CGCTGCAGGG ACGAGCTGGA GGGCCCGGAG CCCAAAGGCG GCAACAAGCT CAAGCAGGCC 960
TCGCAGAAGA GCCAGCGCGC GCAGCAGGTC CTGCACCTGC AGGTACTGCA GCTTCAGCAG 1020
```

Fig. 5F-1

```
GAGAAGCGGC AGCTCCGGCA GGAGCTCGAG AGCCTCATGA AGGAGCAGGA CCTGCTGGAG 1080
ACCAAGCTCA GGTCCTACGA GAGGGAGAAG ACCAGCTTCG GCCCCGCGCT GGAGGAGACC 1140
CAGTGGGAGG TGTGCCAGAA GTCAGGCGAG ATCTCCCTCC TGAAGCAGCA GCTGAAGGAG 1200
TCCCAGACGG AGGTGAACGC CAAGGCTAGC GAGATCCTGG GTCTCAAGGC ACAGCTGAAG 1260
GACACGCGGG GCAAGCTGGA GGGCCTGGAG CTGAGGACCC AGGACCTGGA GGGCGCCCTG 1320
CGCACCAAGG GCCTGGAGCT GGAGGTCTGT GAGAATGAGC TGCAGCAGAG CTACGTGGCC 1380
ATGTACCAGC GGAACCAGCG CCTGGAGAAG GCCCTGCAGC AGCTGGCACG TGGGGACAGC 1440
GCCGGGGAGC CCTTGGAGGT TGACCTGGAA GGGGCTGACA TCCCCTACGA GGACATCATA 1500
GCCACTGAGA TC                                                    1512
```

Fig. 5F-2

```
ATGGGCAGCG TCAGTAGCCT CATCTCCGGC CACAGCTTCC ACAGCAAGCA CTGCCGGGCT 60
TCGCAGTACA AGCTGCGCAA GTCCTCCCAC CTCAAGAAGC TCAACCGGTA TTCCGACGGG 120
CTGCTGAGGT TTGGCTTCTC CCAGGACTCC GGTCACGGCA AGTCCAGCTC CAAAATGGGC 180
AAGAGCGAAG ACTTCTTCTA CATCAAGGTC AGCCAGAAAG CCCGGGGCTC CCATCACCCA 240
GATTACACGG CACTGTCCAG CGGGGATTTA GGGGGCCAGG CTGGGGTGGA CTTTGACCCG 300
TCCACACCCC CCAAGCTCAT GCCCTTCTCC AATCAGCTAG AAATGGGCTC CGAGAAGGGT 360
GCAGTGAGGC CCACAGCCTT CAAGCCTGTG CTGCCACGGT CAGGAGCCAT CCTGCACTCC 420
TCCCCGGAGA GTGCCAGCCA CCAGCTGCAC CCCGCCCCTC CAGACAAGCC CAAGGAGCAG 480
GAGCTGAAGC CTGGCCTGTG CTCTGGGGCG CTGTCAGACT CCGGCCGGAA CTCCATGTCC 540
AGCCTGCCCA CACACAGCAC CAGCAGCAGC TACCAGCTGG ACCCGCTGGT CACACCCGTG 600
GGACCCACAA GCCGTTTTGG GGGCTCCGCC CACAACATCA CCCAGGGCAT CGTCCTCCAG 660
```

Fig. 5G-1

```
GACAGCAACA TGATGAGCCT GAAGGCTCTG TCCTTCTCCG ACGGAGGTAG CAAGCTGGGC 720
CACTCGAACA AGGCAGACAA GGGCCCCTCG TGTGTCCGCT CCCCCATCTC CACGGACGAG 780
TGCAGCATCC AGGAGCTGGA GCAGAAGCTG TTGGAGAGGG AGGGCGCCCT CCAGAAGCTG 840
CAGCGCAGCT TTGAGGAGAA GGAGCTTGCC TCCAGCCTGG CCTACGAGGA GCGGCCGCGG 900
CGCTGCAGGG ACGAGCTGGA GGGCCCGGAG CCCAAAGGCG GCAACAAGCT CAAGCAGGCC 960
TCGCAGAAGA GCCAGCGCGC GCAGCAGGTC CTGCACCTGC AGGTACTGCA GCTTCAGCAG 1020
GAGAAGCGGC AGCTCCGGCA GGAGCTCGAG AGCCTCATGA AGGAGCAGGA CCTGCTGGAG 1080
ACCAAGCTCA GGTCCTACGA GAGGGAGAAG ACCAGCTTCG GCCCCGCGCT GGAGGAGACC 1140
CAGTGGGAGG TGTGCCAGAA GTCAGGCGAG ATCTCCCTCC TGAAGCAGCA GCTGAAGGAG 1200
TCCCAGACGG AGGTGAACGC CAAGGCTAGC GAGATCCTGG GTCTCAAGGC ACAGCTGAAG 1260
GACACGCGGG GCAAGCTGGA GGGCCTGGAG CTGAGGACCC AGGACCTGGA GGGCGCCCTG 1320
CGCACCAAGG GCCTGGAGCT GGAGGTCTGT GAGAATGAGC TGCAGCGCAA GAAGAACGAG 1380
GCGGAGCTGC TGCGGGAGAA GGTGAACCTG CTGGAGCGGC TGCGGGCCGA GCTGCGGGAG 1440
GAGCGGCAAG GCCATGACCA GATGTCCTCG GGCTTCCAGC ATGAGCGGCT CGTGTGGAAG 1500
GAGGAGAAGG AGAAGGTGAT TCAGTACCAG AAACAGCTGC AGCAGAGCTA CGTGGCCATG 1560
TACCAGCGGA ACCAGCGCCT GGAGAAGGCC CTGCAGCAGC TGGCACGTGG GGACAGCGCC 1620
GGGGAGCCCT TGGAGGTTGA CCTGGAAGGG GCTGACATCC CCTACGAGGA CATCATAGCC 1680
ACTGAGATCT GA                                                    1692
```

Fig. 5G-2

```
ATGGGCAGCG TCAGTAGCCT CATCTCCGGC CACAGCTTCC ACAGCAAGCA CTGCCGGGCT 60
TCGCAGTACA AGCTGCGCAA GTCCTCCCAC CTCAAGAAGC TCAACCGGTA TTCCGACGGG 120
CTGCTGAGGT TTGGCTTCTC CCAGGACTCC GGTCACGGCA AGTCCAGCTC CAAAATGGGC 180
```

Fig. 5H-1

AAGAGCGAAG ACTTCTTCTA CATCAAGGTC AGCCAGAAAG CCCGGGGCTC CCATCACCCA 240
GATTACACGG CACTGTCCAG CGGGGATTTA GGGGGCCAGG CTGGGGTGGA CTTTGACCCG 300
TCCACACCCC CCAAGCTCAT GCCCTTCTCC AATCAGCTAG AAATGGGCTC CGAGAAGGGT 360
GCAGTGAGGC CCACAGCCTT CAAGCCTGTG CTGCCACGGT CAGGAGCCAT CCTGCACTCC 420
TCCCCGGAGA GTGCCAGCCA CCAGCTGCAC CCCGCCCCTC CAGACAAGCC CAAGGAGCAG 480
GAGCTGAAGC CTGGCCTGTG CTCTGGGGCG CTGTCAGACT CCGGCCGGAA CTCCATGTCC 540
AGCCTGCCCA CACACAGCAC CAGCAGCAGC TACCAGCTGG ACCCGCTGGT CACACCCGTG 600
GGACCCACAA GCCGTTTTGG GGGCTCCGCC CACAACATCA CCCAGGGCAT CGTCCTCCAG 660
GACAGCAACA TGATGAGCCT GAAGGCTCTG TCCTTCTCCG ACGGAGGTAG CAAGCTGGGC 720
CACTCGAACA AGGCAGACAA GGGCCCCTCG TGTGTCCGCT CCCCCATCTC CACGGACGAG 780
TGCAGCATCC AGGAGCTGGA GCAGAAGCTG TTGGAGAGGG AGGGCGCCCT CCAGAAGCTG 840
CAGCGCAGCT TTGAGGAGAA GGAGCTTGCC TCCAGCCTGG CCTACGAGGA GCGGCCGCGG 900
CGCTGCAGGG ACGAGCTGGA GGGCCCGGAG CCCAAAGGCG GCAACAAGCT CAAGCAGGCC 960
TCGCAGAAGA GCCAGCGCGC GCAGCAGGTC CTGCACCTGC AGGTACTGCA GCTTCAGCAG 1020
GAGAAGCGGC AGCTCCGGCA GGAGCTCGAG AGCCTCATGA AGGAGCAGGA CCTGCTGGAG 1080
ACCAAGCTCA GGTCCTACGA GAGGGAGAAG ACCAGCTTCG GCCCCGCGCT GGAGGAGACC 1140
CAGTGGGAGG TGTGCCAGAA GTCAGGCGAG ATCTCCCTCC TGAAGCAGCA GCTGAAGGAG 1200
TCCCAGACGG AGGTGAACGC CAAGGCTAGC GAGATCCTGG GTCTCAAGGC ACAGCTGAAG 1260
GACACGCGGG GCAAGCTGGA GGGCCTGGAG CTGAGGACCC AGGACCTGGA GGGCGCCCTG 1320
CGCACCAAGG GCCTGGAGCT GGAGGTCTGT GAGAATGAGC TGCAGCGCAA GAAGAACGAG 1380
GCGGAGCTGC TGCGGGAGAA GGTGAACCTG CTGGAGCAGG AGCTGCAGGA GCTGCGGGCC 1440
CAGGCCGCCC TGGCCCGCGA CATGGGGCCG CCCACCTTCC CCGAGGACGT CCCTGCCCTG 1500
CAGCGGGAGC TGGAGCGGCT CGTGTGGAAG GAGGAGAAGG AGAAGGTGAT TCAGTACCAG 1560
AAACAGCTGC AGCAGAGCTA CGTGGCCATG TACCAGCGGA ACCAGCGCCT GGAGAAGGCC 1620
CTGCAGCAGC TGGCACGTGG GGACAGCGCC GGGGAGCCCT TGGAGGTTGA CCTGGAAGGG 1680
GCTGACATCC CCTACGAGGA CATCATAGCC ACTGAGATCT GA 1722

Fig. 5H-2

```
ATGGGCAGCG TCAGTAGCCT CATCTCCGGC CACAGCTTCC ACAGCAAGCA CTGCCGGGCT 60
TCGCAGTACA AGCTGCGCAA GTCCTCCCAC CTCAAGAAGC TCAACCGGTA TTCCGACGGG 120
CTGCTGAGGT TTGGCTTCTC CCAGGACTCC GGTCACGGCA AGTCCAGCTC CAAAATGGGC 180
AAGAGCGAAG ACTTCTTCTA CATCAAGGTC AGCCAGAAAG CCCGGGGCTC CCATCACCCA 240
GATTACACGG CACTGTCCAG CGGGGATTTA GGGGGCCAGG CTGGGGTGGA CTTTGACCCG 300
TCCACACCCC CCAAGCTCAT GCCCTTCTCC AATCAGCTAG AAATGGGCTC CGAGAAGGGT 360
GCAGTGAGGC CCACAGCCTT CAAGCCTGTG CTGCCACGGT CAGGAGCCAT CCTGCACTCC 420
TCCCCGGAGA GTGCCAGCCA CCAGCTGCAC CCCGCCCCTC CAGACAAGCC CAAGGAGCAG 480
GAGCTGAAGC CTGGCCTGTG CTCTGGGGCG CTGTCAGACT CCGGCCGGAA CTCCATGTCC 540
AGCCTGCCCA CACACAGCAC CAGCAGCAGC TACCAGCTGG ACCCGCTGGT CACACCCGTG 600
GGACCCACAA GCCGTTTTGG GGGCTCCGCC CACAACATCA CCCAGGGCAT CGTCCTCCAG 660
GACAGCAACA TGATGAGCCT GAAGGCTCTG TCCTTCTCCG ACGGAGGTAG CAAGCTGGGC 720
CACTCGAACA AGGCAGACAA GGGCCCCTCG TGTGTCCGCT CCCCCATCTC CACGGACGAG 780
TGCAGCATCC AGGAGCTGGA GCAGAAGCTG TTGGAGAGGG AGGGCGCCCT CCAGAAGCTG 840
CAGCGCAGCT TTGAGGAGAA GGAGCTTGCC TCCAGCCTGG CCTACGAGGA GCGGCCGCGG 900
CGCTGCAGGG ACGAGCTGGA GGGCCCGGAG CCCAAAGGCG GCAACAAGCT CAAGCAGGCC 960
TCGCAGAAGA GCCAGCGCGC GCAGCAGGTC CTGCACCTGC AGGTACTGCA GCTTCAGCAG 1020
GAGAAGCGGC AGCTCCGGCA GGAGCTCGAG AGCCTCATGA AGGAGCAGGA CCTGCTGGAG 1080
ACCAAGCTCA GGTCCTACGA GAGGGAGAAG ACCAGCTTCG GCCCCGCGCT GGAGGAGACC 1140
CAGTGGGAGG TGTGCCAGAA GTCAGGCGAG ATCTCCCTCC TGAAGCAGCA GCTGAAGGAG 1200
TCCCAGACGG AGGTGAACGC CAAGGCTAGC GAGATCCTGG GTCTCAAGGC ACAGCTGAAG 1260
GACACGCGGG GCAAGCTGGA GGGCCTGGAG CTGAGGACCC AGGACCTGGA GGGCGCCCTG 1320
CGCACCAAGG GCCTGGAGCT GGAGGTCTGT GAGAATGAGC TGCAGCGCAA GAAGAACGAG 1380
GCGGAGCTGC TGCGGGAGAA GGTGAACCTG CTGGAGCAGG AGCTGCAGGA GCTGCGGGCC 1440
CAGGCCGCCC TGGCCCGCGA CATGGGGCCG CCCACCTTCC CCGAGGACGT CCCTGCCCTG 1500
```

Fig. 5I-1

```
CAGCGGGAGC TGGAGCGGCT GCGGGCCGAG CTGCGGGAGG AGCGGCAAGG CCATGACCAG 1560
ATGTCCTCGG GCTTCCAGCA TGAGCGGCTC GTGTGGAAGG AGGAGAAGGA GAAGGTGATT 1620
CAGTACCAGA AACAGCTGCA GCAGAGCTAC GTGGCCATGT ACCAGCGGAA CCAGCGCCTG 1680
GAGAAGGCCC TGCAGCAGCT GGCACGTGGG GACAGCGCCG GGGAGCCCTT GGAGGTTGAC 1740
CTGGAAGGGG CTGACATCCC CTACGAGGAC ATCATAGCCA CTGAGATCTG A          1791
```

Fig. 5I-2

```
 MET GLY SER VAL SER SER LEU ILE SER GLY HIS SER PHE HIS SER LYS
  1               5                  10                  15

HIS CYS ARG ALA SER GLN TYR LYS LEU ARG LYS SER SER HIS LEU LYS
            20                  25                  30

LYS LEU ASN ARG TYR SER ASP GLY LEU LEU ARG PHE GLY PHE SER GLN
        35                  40                  45

ASP SER GLY HIS GLY LYS SER SER SER LYS MET GLY LYS SER GLU ASP
    50                  55                  60

PHE PHE TYR ILE LYS VAL SER GLN LYS ALA ARG GLY SER HIS HIS PRO
65                  70                  75                  80

ASP TYR THR ALA LEU SER SER GLY ASP LEU GLY GLY GLN ALA GLY VAL
                85                  90                  95

ASP PHE ASP PRO SER THR PRO PRO LYS LEU MET PRO PHE SER ASN GLN
            100                 105                 110

LEU GLU MET GLY SER GLU LYS GLY ALA VAL ARG PRO THR ALA PHE LYS
        115                 120                 125

PRO VAL LEU PRO ARG SER GLY ALA ILE LEU HIS SER SER PRO GLU SER
    130                 135                 140
```

Fig. 5J-1

```
ALA SER HIS GLN LEU HIS PRO ALA PRO PRO ASP LYS PRO LYS GLU GLN
145                 150                 155                 160

GLU LEU LYS PRO GLY LEU CYS SER GLY ALA LEU SER ASP SER GLY ARG
                165                 170                 175

ASN SER MET SER SER LEU PRO THR HIS SER THR SER SER SER TYR GLN
            180                 185                 190

LEU ASP PRO LEU VAL THR PRO VAL GLY PRO THR SER ARG PHE GLY GLY
        195                 200                 205

SER ALA HIS ASN ILE THR GLN GLY ILE VAL LEU GLN ASP SER ASN MET
    210                 215                 220

MET SER LEU LYS ALA LEU SER PHE SER ASP GLY GLY SER LYS LEU GLY
225                 230                 235                 240

HIS SER ASN LYS ALA ASP LYS GLY PRO SER CYS VAL ARG SER PRO ILE
                245                 250                 255

SER THR ASP GLU CYS SER ILE GLN GLU LEU GLU GLN LYS LEU LEU GLU
            260                 265                 270
```

Fig. 5J-2

```
ARG GLU GLY ALA LEU GLN LYS LEU GLN ARG SER PHE GLU GLU LYS GLU
        275                 280                 285

LEU ALA SER SER LEU ALA TYR GLU GLU ARG PRO ARG ARG CYS ARG ASP
    290                 295                 300

GLU LEU GLU GLY PRO GLU PRO LYS GLY GLY ASN LYS LEU LYS GLN ALA
305                 310                 315                 320

SER GLN LYS SER GLN ARG ALA GLN GLN VAL LEU HIS LEU GLN VAL LEU
                325                 330                 335

GLN LEU GLN GLN GLU LYS ARG GLN LEU ARG GLN GLU LEU GLU SER LEU
            340                 345                 350

MET LYS GLU GLN ASP LEU LEU GLU THR LYS LEU ARG SER TYR GLU ARG
        355                 360                 365

GLU LYS THR SER PHE GLY PRO ALA LEU GLU GLU THR GLN TRP GLU VAL
    370                 375                 380

CYS GLN LYS SER GLY GLU ILE SER LEU LEU LYS GLN GLN LEU LYS GLU
385                 390                 395                 400
```

Fig. 5J-3

SER GLN THR GLU VAL ASN ALA LYS ALA SER GLU ILE LEU GLY LEU LYS
405 410 415

ALA GLN LEU LYS ASP THR ARG GLY LYS LEU GLU GLY LEU GLU LEU ARG
420 425 430

THR GLN ASP LEU GLU GLY ALA LEU ARG THR LYS GLY LEU GLU LEU GLU
435 440 445

VAL CYS GLU ASN GLU LEU GLN ARG LYS LYS ASN GLU ALA GLU LEU LEU
450 455 460

ARG GLU LYS VAL ASN LEU LEU GLU GLN GLU LEU GLN GLU LEU ARG ALA
465 470 475 480

GLN ALA ALA LEU ALA ARG ASP MET GLY PRO PRO THR PHE PRO GLU ASP
485 490 495

VAL PRO ALA LEU GLN ARG GLU LEU GLU ARG LEU ARG ALA GLU LEU ARG
500 505 510

GLU GLU ARG GLN GLY HIS ASP GLN MET SER SER GLY PHE GLN HIS GLU
515 520 525

Fig. 5J-4

```
ARG LEU VAL TRP LYS GLU GLU LYS GLU LYS VAL ILE GLN TYR GLN LYS
    530                 535                 540

GLN LEU GLN GLN SER TYR VAL ALA MET TYR GLN ARG ASN GLN ARG LEU
545                 550                 555                 560

GLU LYS ALA LEU GLN GLN LEU ALA ARG GLY ASP SER ALA GLY GLU PRO
                565                 570                 575

LEU GLU VAL ASP LEU GLU GLY ALA ASP ILE PRO TYR GLU ASP ILE ILE
            580                 585                 590

ALA THR GLU ILE
        595
```

Fig. 5J-5

```
MET GLY SER VAL SER SER LEU ILE SER GLY HIS SER PHE HIS SER LYS
  1               5                  10                  15

HIS CYS ARG ALA SER GLN TYR LYS LEU ARG LYS SER SER HIS LEU LYS
            20                  25                  30

LYS LEU ASN ARG TYR SER ASP GLY LEU LEU ARG PHE GLY PHE SER GLN
        35                  40                  45

ASP SER GLY HIS GLY LYS ALA MET THR ARG CYS PRO ARG ALA SER SER
    50                  55                  60

MET SER GLY SER CYS GLY ARG ARG ARG ARG ARG ARG
 65                  70                  75
```

Fig. 5K

```
MET GLY SER VAL SER SER LEU ILE SER GLY HIS SER PHE HIS SER LYS
  1               5                  10                  15

HIS CYS ARG ALA SER GLN TYR LYS LEU ARG LYS SER SER HIS LEU LYS
            20                  25                  30

LYS LEU ASN ARG TYR SER ASP GLY LEU LEU ARG PHE GLY PHE SER GLN
        35                  40                  45

ASP SER GLY HIS GLY LYS SER SER SER LYS MET GLY LYS SER GLU ASP
    50                  55                  60

PHE PHE TYR ILE LYS VAL SER GLN LYS ALA ARG GLY SER HIS HIS PRO
65                  70                  75                  80

ASP TYR THR ALA LEU SER SER GLY ASP LEU GLY GLY GLN ALA GLY VAL
                85                  90                  95

ASP PHE ASP PRO SER THR PRO PRO LYS LEU MET PRO PHE SER ASN GLN
            100                 105                 110

LEU GLU MET GLY SER GLU LYS GLY ALA VAL ARG PRO THR ALA PHE LYS
        115                 120                 125

PRO VAL LEU PRO ARG SER GLY ALA ILE LEU HIS SER SER PRO GLU SER
    130                 135                 140
```

Fig. 5L-1

```
ALA SER HIS GLN LEU HIS PRO ALA PRO PRO ASP LYS PRO LYS GLU GLN
145                 150                 155                 160

GLU LEU LYS PRO GLY LEU CYS SER GLY ALA LEU SER ASP SER GLY ARG
                165                 170                 175

ASN SER MET SER SER LEU PRO THR HIS SER ALA GLY GLU PRO LEU GLU
            180                 185                 190

VAL ASP LEU GLU GLY ALA ASP ILE PRO TYR GLU ASP ILE ILE ALA THR
        195                 200                 205

GLU ILE
    210
```

Fig. 5L-2

```
MET GLY SER VAL SER SER LEU ILE SER GLY HIS SER PHE HIS SER LYS
  1               5                  10                  15

HIS CYS ARG ALA SER GLN TYR LYS LEU ARG LYS SER SER HIS LEU LYS
            20                  25                  30

LYS LEU ASN ARG TYR SER ASP GLY LEU LEU ARG PHE GLY PHE SER GLN
        35                  40                  45

ASP SER GLY HIS GLY LYS SER SER SER LYS MET GLY LYS SER GLU ASP
    50                  55                  60

PHE PHE TYR ILE LYS VAL SER GLN LYS ALA ARG GLY SER HIS HIS PRO
65                  70                  75                  80

ASP TYR THR ALA LEU SER SER GLY ASP LEU GLY GLY GLN ALA GLY VAL
                85                  90                  95

ASP PHE ASP PRO SER THR PRO PRO LYS LEU MET PRO PHE SER ASN GLN
            100                 105                 110

LEU GLU MET GLY SER GLU LYS GLY ALA VAL ARG PRO THR ALA PHE LYS
        115                 120                 125

PRO VAL LEU PRO ARG SER GLY ALA ILE LEU HIS SER SER PRO GLU SER
    130                 135                 140
```

Fig. 5M-1

```
ALA SER HIS GLN LEU HIS PRO ALA PRO PRO ASP LYS PRO LYS GLU GLN
145                 150                 155                 160

GLU LEU LYS PRO GLY LEU CYS SER GLY ALA LEU SER ASP SER GLY ARG
            165                 170                 175

ASN SER MET SER SER LEU PRO THR HIS SER THR SER SER SER TYR GLN
        180                 185                 190

LEU ASP PRO LEU VAL THR PRO VAL GLY PRO THR SER ARG PHE GLY GLY
    195                 200                 205

SER ALA HIS ASN ILE THR GLN GLY ILE VAL LEU GLN ASP SER ASN MET
210                 215                 220

MET SER LEU LYS ALA LEU SER PHE SER ASP GLY GLY SER LYS LEU GLY
225                 230                 235                 240

HIS SER ASN LYS ALA ASP LYS GLY PRO SER CYS VAL ARG SER PRO ILE
            245                 250                 255

SER THR ASP GLU CYS SER ILE GLN GLU LEU GLU GLN LYS LEU LEU GLU
        260                 265                 270
```

Fig. 5M-2

```
ARG GLU GLY ALA LEU GLN LYS LEU GLN ARG SER PHE GLU GLU LYS GLU
        275                 280                 285

LEU ALA SER SER LEU ALA TYR GLU GLU ARG PRO ARG ARG CYS ARG ASP
    290                 295                 300

GLU LEU GLU GLY PRO GLU PRO LYS GLY GLY ASN LYS LEU LYS GLN ALA
305                 310                 315                 320

SER GLN LYS SER GLN ARG ALA GLN GLN VAL LEU HIS LEU GLN VAL LEU
                325                 330                 335

GLN LEU GLN GLN GLU LYS ARG GLN LEU ARG GLN GLU LEU GLU SER LEU
            340                 345                 350

MET LYS GLU GLN ASP LEU LEU GLU THR LYS LEU ARG SER TYR GLU ARG
        355                 360                 365

GLU LYS THR SER PHE GLY PRO ALA LEU GLU GLU THR GLN TRP GLU VAL
    370                 375                 380

CYS GLN LYS SER GLY GLU ILE SER LEU LEU LYS GLN GLN LEU LYS GLU
385                 390                 395                 400
```

Fig. 5M-3

```
SER GLN THR GLU VAL ASN ALA LYS ALA SER GLU ILE LEU GLY LEU LYS
                405                 410                 415

ALA GLN LEU LYS ASP THR ARG GLY LYS LEU GLU GLY LEU GLU LEU ARG
            420                 425                 430

THR GLN ASP LEU GLU GLY ALA LEU ARG THR LYS GLY LEU GLU LEU GLU
        435                 440                 445

VAL CYS GLU ASN GLU LEU GLN ARG LYS LYS ASN GLU ALA GLU LEU LEU
    450                 455                 460

ARG GLU LYS HIS GLU ARG LEU VAL TRP LYS GLU GLU LYS GLU LYS VAL
465                 470                 475                 480

ILE GLN TYR GLN LYS GLN LEU GLN GLN SER TYR VAL ALA MET TYR GLN
                485                 490                 495

ARG ASN GLN ARG LEU GLU LYS ALA LEU GLN GLN LEU ALA ARG GLY ASP
            500                 505                 510

SER ALA GLY GLU PRO LEU GLU VAL ASP LEU GLU GLY ALA ASP ILE PRO
        515                 520                 525

TYR GLU ASP ILE ILE ALA THR GLU ILE
    530                 535
```

Fig. 5M-4

```
MET GLY SER VAL SER SER LEU ILE SER GLY HIS SER PHE HIS SER LYS
  1               5                  10                  15

HIS CYS ARG ALA SER GLN TYR LYS LEU ARG LYS SER SER HIS LEU LYS
            20                  25                  30

LYS LEU ASN ARG TYR SER ASP GLY LEU LEU ARG PHE GLY PHE SER GLN
        35                  40                  45

ASP SER GLY HIS GLY LYS SER SER SER LYS MET GLY LYS SER GLU ASP
    50                  55                  60

PHE PHE TYR ILE LYS VAL SER GLN LYS ALA ARG GLY SER HIS HIS PRO
65                  70                  75                  80

ASP TYR THR ALA LEU SER SER GLY ASP LEU GLY GLY GLN ALA GLY VAL
                85                  90                  95

ASP PHE ASP PRO SER THR PRO PRO LYS LEU MET PRO PHE SER ASN GLN
            100                 105                 110

LEU GLU MET GLY SER GLU LYS GLY ALA VAL ARG PRO THR ALA PHE LYS
        115                 120                 125

PRO VAL LEU PRO ARG SER GLY ALA ILE LEU HIS SER SER PRO GLU SER
    130                 135                 140
```

Fig. 5N-1

```
ALA SER HIS GLN LEU HIS PRO ALA PRO PRO ASP LYS PRO LYS GLU GLN
145                 150                 155                 160

GLU LEU LYS PRO GLY LEU CYS SER GLY ALA LEU SER ASP SER GLY ARG
                165                 170                 175

ASN SER MET SER SER LEU PRO THR HIS SER THR SER SER SER TYR GLN
            180                 185                 190

LEU ASP PRO LEU VAL THR PRO VAL GLY PRO THR SER ARG PHE GLY GLY
        195                 200                 205

SER ALA HIS ASN ILE THR GLN GLY ILE VAL LEU GLN ASP SER ASN MET
    210                 215                 220

MET SER LEU LYS ALA LEU SER PHE SER ASP GLY GLY SER LYS LEU GLY
225                 230                 235                 240

HIS SER ASN LYS ALA ASP LYS GLY PRO SER CYS VAL ARG SER PRO ILE
                245                 250                 255

SER THR ASP GLU CYS SER ILE GLN GLU LEU GLU GLN LYS LEU LEU GLU
            260                 265                 270
```

Fig. 5N-2

```
ARG GLU GLY ALA LEU GLN LYS LEU GLN ARG SER PHE GLU GLU LYS GLU
        275                 280                 285

LEU ALA SER SER LEU ALA TYR GLU GLU ARG PRO ARG ARG CYS ARG ASP
    290                 295                 300

GLU LEU GLU GLY PRO GLU PRO LYS GLY GLY ASN LYS LEU LYS GLN ALA
305                 310                 315                 320

SER GLN LYS SER GLN ARG ALA GLN GLN VAL LEU HIS LEU GLN VAL LEU
                325                 330                 335

GLN LEU GLN GLN GLU LYS ARG GLN LEU ARG GLN GLU LEU GLU SER LEU
            340                 345                 350

MET LYS GLU GLN ASP LEU LEU GLU THR LYS LEU ARG SER TYR GLU ARG
        355                 360                 365

GLU LYS THR SER PHE GLY PRO ALA LEU GLU GLU THR GLN TRP GLU VAL
    370                 375                 380

CYS GLN LYS SER GLY GLU ILE SER LEU LEU LYS GLN GLN LEU LYS GLU
385                 390                 395                 400
```

Fig. 5N-3

```
SER GLN THR GLU VAL ASN ALA LYS ALA SER GLU ILE LEU GLY LEU LYS
                405                 410                 415

ALA GLN LEU LYS ASP THR ARG GLY LYS LEU GLU GLY LEU GLU LEU ARG
            420                 425                 430

THR GLN ASP LEU GLU GLY ALA LEU ARG THR LYS GLY LEU GLU LEU GLU
        435                 440                 445

VAL CYS GLU ASN GLU LEU GLN GLN SER TYR VAL ALA MET TYR GLN ARG
    450                 455                 460

ASN GLN ARG LEU GLU LYS ALA LEU GLN GLN LEU ALA ARG GLY ASP SER
465                 470                 475                 480

ALA GLY GLU PRO LEU GLU VAL ASP LEU GLU GLY ALA ASP ILE PRO TYR
                485                 490                 495

GLU ASP ILE ILE ALA THR GLU ILE
            500
```

Fig. 5N-4

```
MET GLY SER VAL SER SER LEU ILE SER GLY HIS SER PHE HIS SER LYS
 1               5                  10                  15

HIS CYS ARG ALA SER GLN TYR LYS LEU ARG LYS SER SER HIS LEU LYS
            20                  25                  30

LYS LEU ASN ARG TYR SER ASP GLY LEU LEU ARG PHE GLY PHE SER GLN
        35                  40                  45

ASP SER GLY HIS GLY LYS SER SER SER LYS MET GLY LYS SER GLU ASP
    50                  55                  60

PHE PHE TYR ILE LYS VAL SER GLN LYS ALA ARG GLY SER HIS HIS PRO
65                  70                  75                  80

ASP TYR THR ALA LEU SER SER GLY ASP LEU GLY GLY GLN ALA GLY VAL
                85                  90                  95

ASP PHE ASP PRO SER THR PRO PRO LYS LEU MET PRO PHE SER ASN GLN
            100                 105                 110

LEU GLU MET GLY SER GLU LYS GLY ALA VAL ARG PRO THR ALA PHE LYS
        115                 120                 125

PRO VAL LEU PRO ARG SER GLY ALA ILE LEU HIS SER SER PRO GLU SER
    130                 135                 140
```

Fig. 5O-1

```
ALA SER HIS GLN LEU HIS PRO ALA PRO PRO ASP LYS PRO LYS GLU GLN
145                 150                 155                 160

GLU LEU LYS PRO GLY LEU CYS SER GLY ALA LEU SER ASP SER GLY ARG
                165                 170                 175

ASN SER MET SER SER LEU PRO THR HIS SER THR SER SER SER TYR GLN
            180                 185                 190

LEU ASP PRO LEU VAL THR PRO VAL GLY PRO THR SER ARG PHE GLY GLY
        195                 200                 205

SER ALA HIS ASN ILE THR GLN GLY ILE VAL LEU GLN ASP SER ASN MET
    210                 215                 220

MET SER LEU LYS ALA LEU SER PHE SER ASP GLY GLY SER LYS LEU GLY
225                 230                 235                 240

HIS SER ASN LYS ALA ASP LYS GLY PRO SER CYS VAL ARG SER PRO ILE
                245                 250                 255

SER THR ASP GLU CYS SER ILE GLN GLU LEU GLU GLN LYS LEU LEU GLU
            260                 265                 270
```

Fig. 5O-2

```
ARG GLU GLY ALA LEU GLN LYS LEU GLN ARG SER PHE GLU GLU LYS GLU
        275                 280                 285

LEU ALA SER SER LEU ALA TYR GLU GLU ARG PRO ARG ARG CYS ARG ASP
    290                 295                 300

GLU LEU GLU GLY PRO GLU PRO LYS GLY GLY ASN LYS LEU LYS GLN ALA
305                 310                 315                 320

SER GLN LYS SER GLN ARG ALA GLN GLN VAL LEU HIS LEU GLN VAL LEU
                325                 330                 335

GLN LEU GLN GLN GLU LYS ARG GLN LEU ARG GLN GLU LEU GLU SER LEU
            340                 345                 350

MET LYS GLU GLN ASP LEU LEU GLU THR LYS LEU ARG SER TYR GLU ARG
        355                 360                 365

GLU LYS THR SER PHE GLY PRO ALA LEU GLU GLU THR GLN TRP GLU VAL
    370                 375                 380

CYS GLN LYS SER GLY GLU ILE SER LEU LEU LYS GLN GLN LEU LYS GLU
385                 390                 395                 400
```

Fig. 5O-3

```
SER GLN THR GLU VAL ASN ALA LYS ALA SER GLU ILE LEU GLY LEU LYS
                405                 410                 415

ALA GLN LEU LYS ASP THR ARG GLY LYS LEU GLU GLY LEU GLU LEU ARG
            420                 425                 430

THR GLN ASP LEU GLU GLY ALA LEU ARG THR LYS GLY LEU GLU LEU GLU
        435                 440                 445

VAL CYS GLU ASN GLU LEU GLN ARG LYS LYS ASN GLU ALA GLU LEU LEU
    450                 455                 460

ARG GLU LYS VAL ASN LEU LEU GLU ARG LEU ARG ALA GLU LEU ARG GLU
465                 470                 475                 480

GLU ARG GLN GLY HIS ASP GLN MET SER SER GLY PHE GLN HIS GLU ARG
                485                 490                 495

LEU VAL TRP LYS GLU GLU LYS GLU LYS VAL ILE GLN TYR GLN LYS GLN
            500                 505                 510

LEU GLN GLN SER TYR VAL ALA MET TYR GLN ARG ASN GLN ARG LEU GLU
        515                 520                 525
```

Fig. 5O-4

```
LYS ALA LEU GLN GLN LEU ALA ARG GLY ASP SER ALA GLY GLU PRO LEU
    530                 535                 540

GLU VAL ASP LEU GLU GLY ALA ASP ILE PRO TYR GLU ASP ILE ILE ALA
545                 550                 555                 560

THR GLU ILE
```

Fig. 5O-5

```
MET GLY SER VAL SER SER LEU ILE SER GLY HIS SER PHE HIS SER LYS
  1               5                  10                  15

HIS CYS ARG ALA SER GLN TYR LYS LEU ARG LYS SER SER HIS LEU LYS
            20                  25                  30

LYS LEU ASN ARG TYR SER ASP GLY LEU LEU ARG PHE GLY PHE SER GLN
        35                  40                  45

ASP SER GLY HIS GLY LYS SER SER SER LYS MET GLY LYS SER GLU ASP
    50                  55                  60
```

Fig. 5P-1

```
PHE PHE TYR ILE LYS VAL SER GLN LYS ALA ARG GLY SER HIS HIS PRO
 65                  70                  75                  80

ASP TYR THR ALA LEU SER SER GLY ASP LEU GLY GLY GLN ALA GLY VAL
                 85                  90                  95

ASP PHE ASP PRO SER THR PRO PRO LYS LEU MET PRO PHE SER ASN GLN
            100                 105                 110

LEU GLU MET GLY SER GLU LYS GLY ALA VAL ARG PRO THR ALA PHE LYS
        115                 120                 125

PRO VAL LEU PRO ARG SER GLY ALA ILE LEU HIS SER SER PRO GLU SER
    130                 135                 140

ALA SER HIS GLN LEU HIS PRO ALA PRO PRO ASP LYS PRO LYS GLU GLN
145                 150                 155                 160

GLU LEU LYS PRO GLY LEU CYS SER GLY ALA LEU SER ASP SER GLY ARG
                165                 170                 175

ASN SER MET SER SER LEU PRO THR HIS SER THR SER SER SER TYR GLN
            180                 185                 190
```

Fig. 5P-2

```
LEU ASP PRO LEU VAL THR PRO VAL GLY PRO THR SER ARG PHE GLY GLY
        195                 200                 205

SER ALA HIS ASN ILE THR GLN GLY ILE VAL LEU GLN ASP SER ASN MET
    210                 215                 220

MET SER LEU LYS ALA LEU SER PHE SER ASP GLY GLY SER LYS LEU GLY
225                 230                 235                 240

HIS SER ASN LYS ALA ASP LYS GLY PRO SER CYS VAL ARG SER PRO ILE
                245                 250                 255

SER THR ASP GLU CYS SER ILE GLN GLU LEU GLU GLN LYS LEU LEU GLU
            260                 265                 270

ARG GLU GLY ALA LEU GLN LYS LEU GLN ARG SER PHE GLU GLU LYS GLU
        275                 280                 285

LEU ALA SER SER LEU ALA TYR GLU GLU ARG PRO ARG ARG CYS ARG ASP
    290                 295                 300

GLU LEU GLU GLY PRO GLU PRO LYS GLY GLY ASN LYS LEU LYS GLN ALA
305                 310                 315                 320
```

Fig. 5P-3

```
SER GLN LYS SER GLN ARG ALA GLN GLN VAL LEU HIS LEU GLN VAL LEU
                325                 330                 335

GLN LEU GLN GLN GLU LYS ARG GLN LEU ARG GLN GLU LEU GLU SER LEU
            340                 345                 350

MET LYS GLU GLN ASP LEU LEU GLU THR LYS LEU ARG SER TYR GLU ARG
        355                 360                 365

GLU LYS THR SER PHE GLY PRO ALA LEU GLU GLU THR GLN TRP GLU VAL
    370                 375                 380

CYS GLN LYS SER GLY GLU ILE SER LEU LEU LYS GLN GLN LEU LYS GLU
385                 390                 395                 400

SER GLN THR GLU VAL ASN ALA LYS ALA SER GLU ILE LEU GLY LEU LYS
                405                 410                 415

ALA GLN LEU LYS ASP THR ARG GLY LYS LEU GLU GLY LEU GLU LEU ARG
            420                 425                 430

THR GLN ASP LEU GLU GLY ALA LEU ARG THR LYS GLY LEU GLU LEU GLU
        435                 440                 445
```

Fig. 5P-4

```
VAL CYS GLU ASN GLU LEU GLN ARG LYS LYS ASN GLU ALA GLU LEU LEU
    450                 455                 460

ARG GLU LYS VAL ASN LEU LEU GLU GLN GLU LEU GLN GLU LEU ARG ALA
465                 470                 475                 480

GLN ALA ALA LEU ALA ARG ASP MET GLY PRO PRO THR PHE PRO GLU ASP
                485                 490                 495

VAL PRO ALA LEU GLN ARG GLU LEU GLU ARG LEU VAL TRP LYS GLU GLU
            500                 505                 510

LYS GLU LYS VAL ILE GLN TYR GLN LYS GLN LEU GLN GLN SER TYR VAL
        515                 520                 525

ALA MET TYR GLN ARG ASN GLN ARG LEU GLU LYS ALA LEU GLN GLN LEU
    530                 535                 540

ALA ARG GLY ASP SER ALA GLY GLU PRO LEU GLU VAL ASP LEU GLU GLY
545                 550                 555                 560

ALA ASP ILE PRO TYR GLU ASP ILE ILE ALA THR GLU ILE
                565                 570
```

Fig. 5P-5

```
GGACTCTGCC CCTGGACCTG GGAACGACTG GACTGTCACG GGGTTCCCTC CTAGCTCTCC  60
CAGTGAACTC CTGCCAGGCA CACACAGCCC CTATAGCACT GAGCTCACAT GGGACTGGGA 120
TATGGGGGCA TCTCTTCCCC AGAGAGGCAC TCAGTGAGCC TCCTGTGCCT GGCCCCAGTC 180
TGGGCCATCT CTTAGGTGAG ACAGTTGCCC GAAACTAAGC CAGGCCTGGC TGGAGGAGCA 240
GCAGCTTGGG GAGAGGGATT TCCCTGCAGA CCTCAAGCCA TCATGCGGTG GGTGCTGCCA 300
TGACAGAGGC TGCACCCCTG GGCCAGCGGG GCTGCTCACC CACCTCTTGT GCAAGGTGGC 360
CTTTGTGCTG CGCCTGCAGG CAGAGCTGGA GCCCCCAGCA GAGGCAGGCT GGGACGGACC 420
AGCATCTGGA AGATGTACAT AGTTATTTTT CTCTTTGTGG TTTCTTGTTT GGTTTGGTTT 480
GCTTTTGACA GCTTCATTTT ATTTTTGACG TCACTTTTTG GCCATGTAAA CTATTTGTGG 540
CAATTTTATG TTTTTATTTA TGAATAAAGA ATGCCATTTC TCACGCCCTC T          591
```

Fig. 5Q

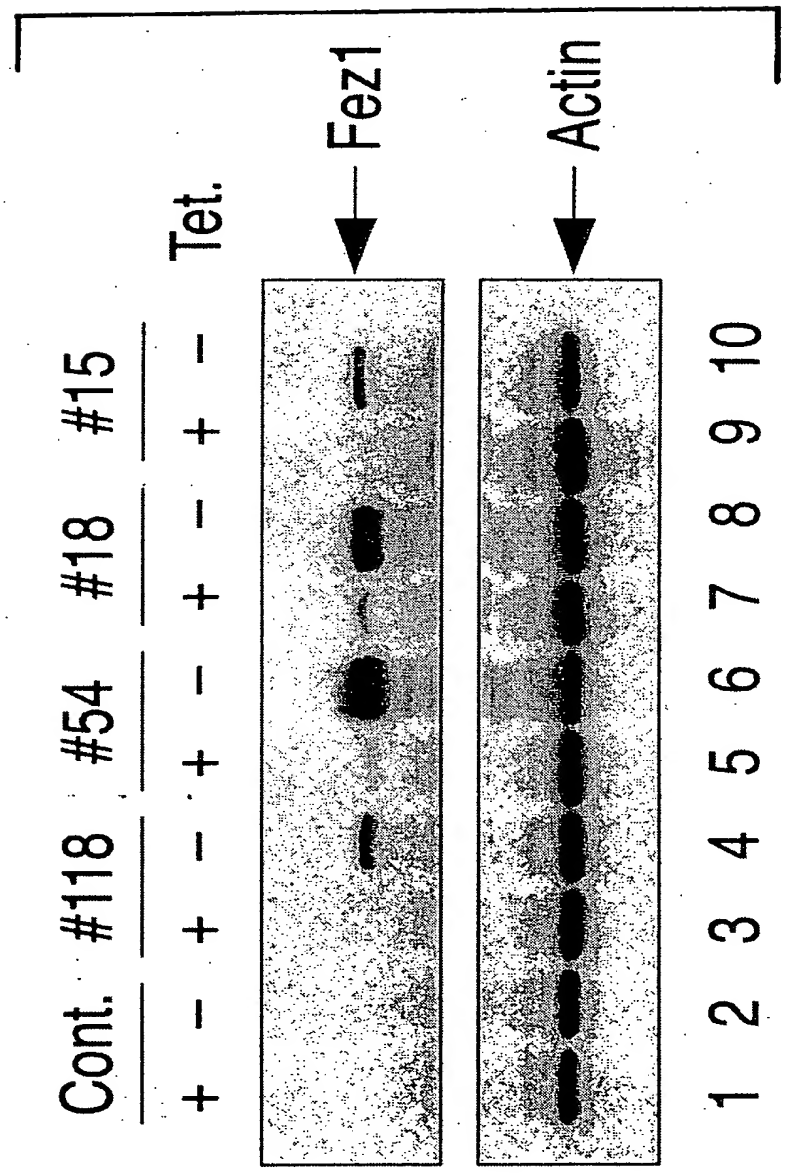


FIG. 6

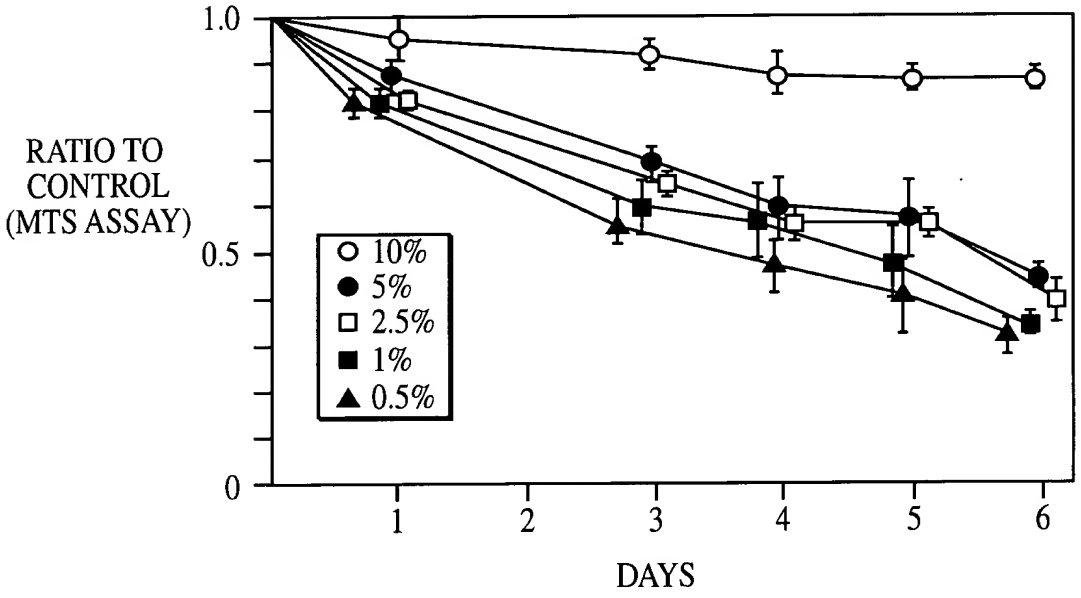

1.0
0.5
0
RATIO TO CONTROL (MTS ASSAY)
10%
5%
2.5%
1%
0.5%
1
2
3
4
5
6
DAYS

Fig. 7A

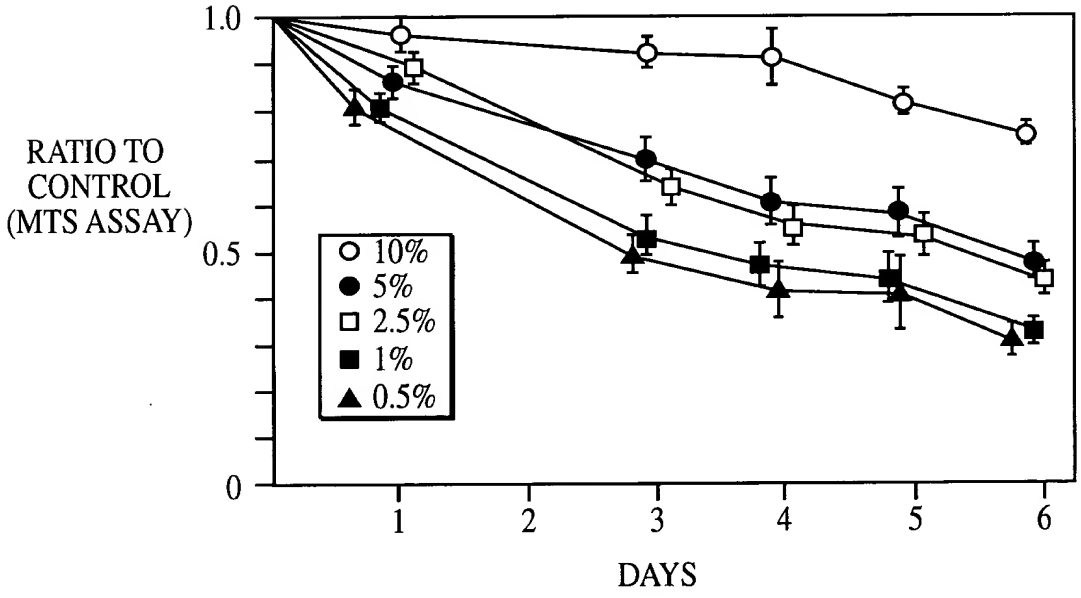

1.0
0.5
0
RATIO TO CONTROL (MTS ASSAY)
10%
5%
2.5%
1%
0.5%
1
2
3
4
5
6
DAYS

Fig. 7B

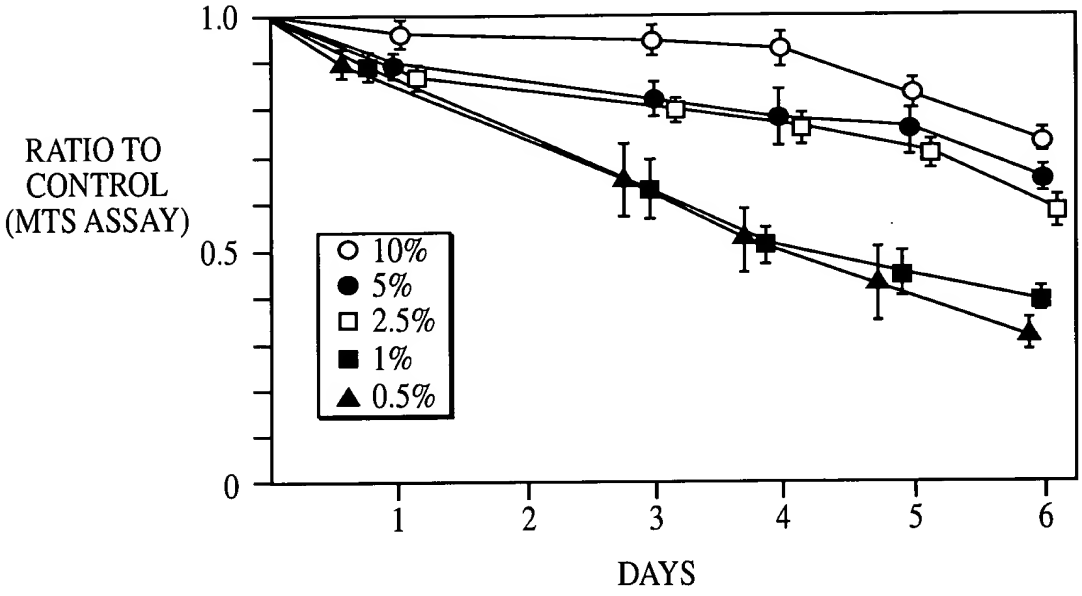

1.0
0.5
0
RATIO TO CONTROL (MTS ASSAY)
10%
5%
2.5%
1%
0.5%
1
2
3
4
5
6
DAYS

Fig. 7C

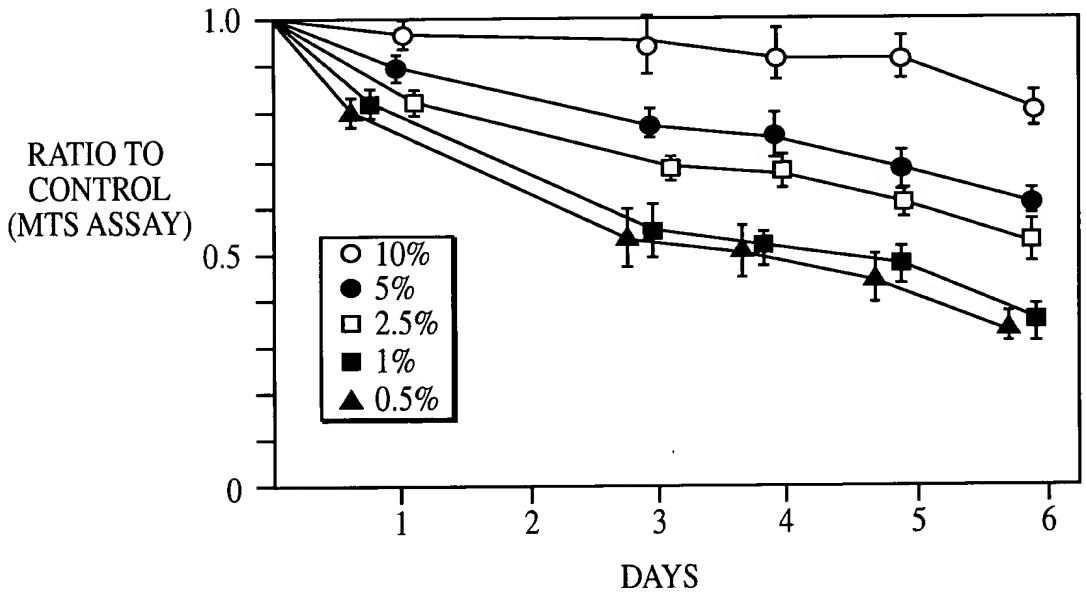

1.0
0.5
0
RATIO TO CONTROL (MTS ASSAY)
10%
5%
2.5%
1%
0.5%
1
2
3
4
5
6
DAYS

Fig. 7D

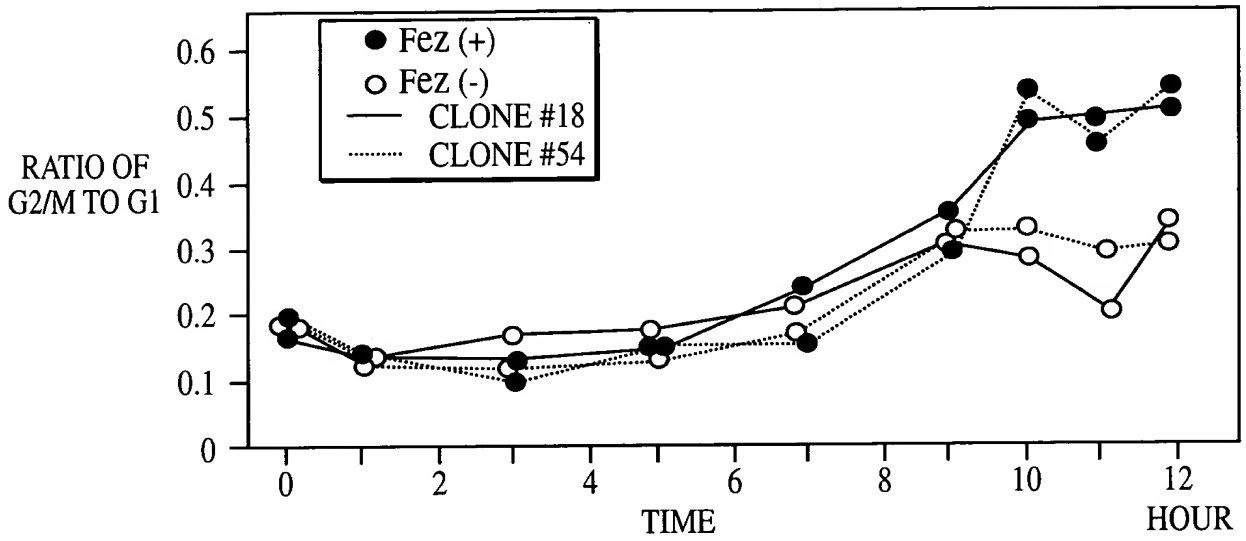

Fez (+)
Fez (-)
CLONE #18
CLONE #54
RATIO OF G2/M TO G1
0.6
0.5
0.4
0.3
0.2
0.1
0
0
2
4
6
8
10
12
TIME
HOUR

Fig. 8A

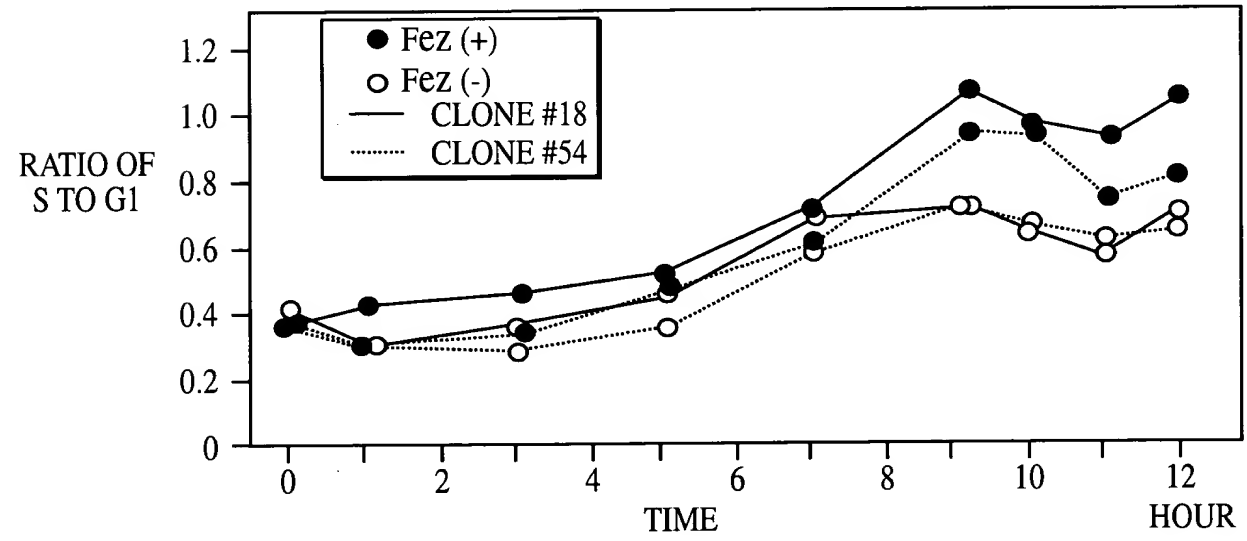

Fez (+)
Fez (-)
CLONE #18
CLONE #54
RATIO OF S TO G1
1.2
1.0
0.8
0.6
0.4
0.2
0
0
2
4
6
8
10
12
TIME
HOUR

Fig. 8B

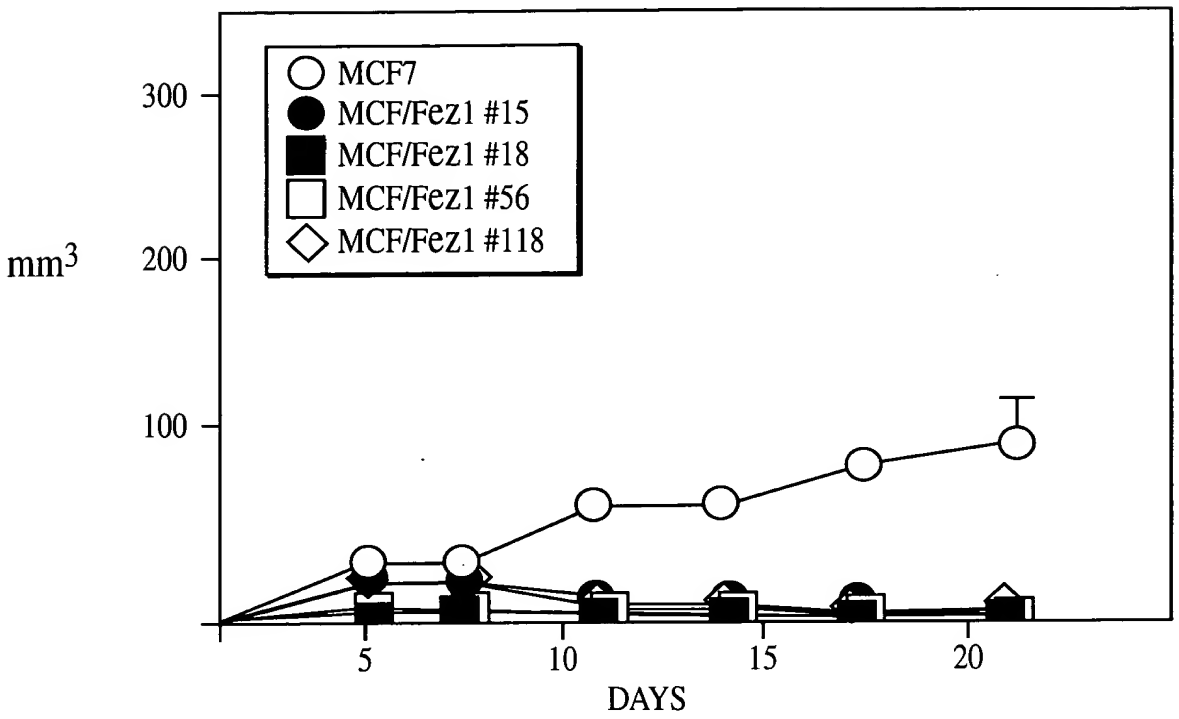

MCF7
MCF/Fez1 #15
MCF/Fez1 #18
MCF/Fez1 #56
MCF/Fez1 #118
300
200
100
mm3
5
10
15
20
DAYS

Fig. 9A

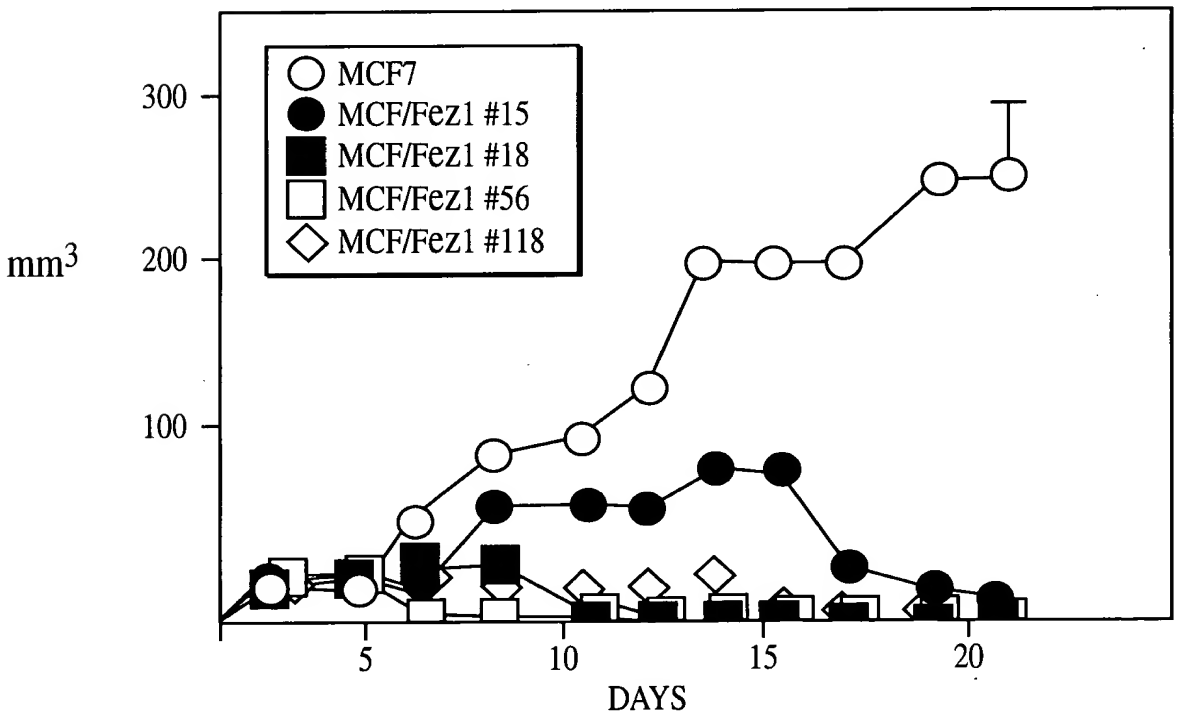

MCF7
MCF/Fez1 #15
MCF/Fez1 #18
MCF/Fez1 #56
MCF/Fez1 #118
300
200
100
mm3
5
10
15
20
DAYS

Fig. 9B

```
   1 GAATTCGGCC GGCCATCATC AATAATATAC CTTATTTTGG ATTGAAGCCA ATATGATAAT
  61 GAGGGGGTGG AGTTTGTGAC GTGGCGCGGG GCGTGGGAAC GGGGCGGGTG ACGTAGTAGT
 121 GTGGCGGAAG TGTGATGTTG CAAGTGTGGC GGAACACATG TAAGCGACGG ATGTGGCAAA
 181 AGTGACGTTT TTGGTGTGCG CCGGTGTACA CAGGAAGTGA CAATTTTCGC GCGGTTTTAG
 241 GCGGATGTTG TAGTAAATTT GGGCGTAACC GAGTAAGATT TGGCCATTTT CGCGGGAAAA
 301 CTGAATAAGA GGAAGTGAAA TCTGAATAAT TTTGTGTTAC TCATAGCGCG TAATATTTGT
 361 CTAGGGCCGC CAGATCGATC TCCGAGGGAT CTCGACCAAA TGATTTGCCC TCCCATATGT
 421 CCTTCCGAGT GAGAGACACA AAAAATTCCA ACACACTATT GCAATGAAAA TAAATTTCCT
 481 TTATTAGCCA GAGGTCGAGG TCGGGGGATC CTCAGTTGTA CAGTTCATCC ATGCCATGTG
 541 TAATCCCAGC AGCTGTTACA AACTCAAGAA GGACCATGTG GTCTCTCTTT TCGTTGGGAT
 601 CTTTCGAAAG GGCAGATTGT GTGGACAGGT AATGGTTGTC TGGTAAAAGG ACAGGGCCAT
 661 CGCCAATTGG AGTATTTTGT TGATAATGGT CTGCTAGTTG AACGCTTCCA TCTTCAATGT
 721 TGTGGCGGGT CTTGAAGTTC ACTTTGATTC CATTCTTTTG TTTGTCTGCC ATGATGTATA
 781 CATTGTGTGA GTTATAGTTG TATTCCAATT TGTGTCCCAG AATGTTGCCA TCTTCCTTGA
 841 AGTCAATACC TTTTAACTCG ATTCTATTAA CAAGGGTATC ACCTTCAAAC TTGACTTCAG
 901 CACGTGTCTT GTAGTTGCCG TCATCTTTGA AGAAGATGGT CCTTTCCTGT ACATAACCTT
 961 CGGGCATGGC ACTCTTGAAA AAGTCATGCC GTTTCATATG ATCCGGGTAT CTTGAAAAGC
1021 ATTGAACACC ATAGCACAGA GTAGTGACTA GTGTTGGCCA TGGAACAGGC AGTTTGCCAG
1081 TAGTGCAGAT GAACTTCAGG GTAAGTTTTC CGTATGTTGC ATCACCTTCA CCCTCTCCAC
1141 TGACAGAGAA CTTGTGGCCG TTAACATCAC CATCTAATTC AACAAGAATT GGGACAACTC
1201 CAGTGAAGAG TTCTTCTCCT TTGCTAGCCA TGGCGGATCC GGCTGAACGG TCTGGTTATA
1261 GGTACATTGA GCAACTGACT GAAATGCCTC AAAATGTTCT TTACGATGCC ATTGGGATAT
1321 ATCAACGGTG GTATATCCAG TGATTTTTTT CTCCATGGTT GTGGCAAGCT TATCATCGTG
1381 TTTTTCAAAG GAAAACCACG TCCCCGTGGT TCGGGGGGCC TAGACGTTTT TTAACCTCGA
1441 CTAAACACAT GTAAAGCATG TGCACCGAGG CCCCAGATCA GATCCCATAC AATGGGGTAC
```

Fig. 10A

1501	CTTCTGGGCA	TCCTTCAGCC	CCTTGTTGAA	TACGCTTGAG	GAGAGCCATT	TGACTCTTTC
1561	CACAACTATC	CAACTCACAA	CGTGGCACTG	GGGTTGTGCC	GCCTTTGCAG	GTGTATCTTA
1621	TACACGTGGC	TTTTGGCCGC	AGAGGCACCT	GTCGCCAGGT	GGGGGGTTCC	GCTGCCTGCA
1681	AAGGGTCGCT	ACAGACGTTG	TTTGTCTTCA	AGAAGCTTCC	AGAGGAACTG	CTTCCTTCAC
1741	GACATTCAAC	AGACCTTGCA	TTCCTTTGGC	GAGAGGGGAA	AGACCCCTAG	GAATGCTCGT
1801	CAAGAAGACA	GGGCCAGGTT	TCCGGGCCCT	CACATTGCCA	AAAGACGGCA	ATATGGTGGA
1861	AAATAACATA	TAGACAAACG	CACACCGGCC	TTATTCCAAG	CGGCTTCGGC	CAGTAACGTT
1921	AGGGGGGGGG	GAGGGAGAGG	GCGGAATTCG	GAGAGGGCGG	AATTCGGGGC	CGCGGAGATC
1981	TTCCAAACTT	GGACCTGGGA	GTGGACACCT	GTGGAGAGAA	AGGCAAAGTG	GATGTCATTG
2041	TCACTCAAGT	GTATGGCCAG	ATCGGGCCAG	GTGAATATCA	AATCCTCCTC	GTTTTTGGAA
2101	ACTGACAATC	TTAGCGCAGA	AGTCATGCCC	GCTTTTGAGA	GGGAGTACTC	ACCCCAACAG
2161	CTGGATCTCA	AGCCTGCCAC	ACCTCACCTC	GACCATCCGC	CGGCTCAAGA	CCGCCTACTT
2221	TAATTACATC	ATCAGCAGCA	CCTCCGCCAG	AAACAACCCC	GACCGCCACC	CGCTGCCGCC
2281	CGCCACGGTG	CTCAGCCTAC	CTTGCGACTG	TGACTGGTTA	GACGCCTTTC	TCGAGAGGTT
2341	TTCCGATCCG	GTCGATGCGG	ACTGGCTCAG	GTCCCTCGGT	GGCGGAGTAC	CGTTCGGAGG
2401	CCGACGGGTT	TCCGATCCAA	GAGTACTGGA	AAGACCGCGA	AGAGTTTGTC	CTCAACCGCG
2461	AGCCCAACAG	CTGGCCCTCG	CAGACAGCGA	TGCGGAAGAG	AGTGAGGATC	TGACGGTTCA
2521	CTAAACGAGC	TCTGCTTATA	TAGACCTCCC	ACCGTACACG	CCTACCGCCC	ATTTGCGTCA
2581	ACGGGGCGGG	GTTATTACGA	CATTTTGGAA	AGTCCCGTTG	ATTTTGGTGC	CAAAACAAAC
2641	TCCCATTGAC	GTCAATGGGG	TGGAGACTTG	GAAATCCCCG	TGAGTCAAAC	CGCTATCCAC
2701	GCCCATTGGT	GTACTGCCAA	AACCGCATCA	CCATGGTAAT	AGCGATGACT	AATACGTAGA
2761	TGTACTGCCA	AGTAGGAAAG	TCCCGTAAGG	TCATGTACTG	GGCATAATGC	CAGGCGGGCC
2821	ATTTACCGTC	ATTGACGTCA	ATAGGGGGCG	GACTTGGCAT	ATGATACACT	TGATGTACTG
2881	CCAAGTGGGC	AGTTTACCGT	AAATACTCCA	CCCATTGACG	TCAATGGAAA	GTCCCTATTG
2941	GCGTTACTAT	GGGAACATAC	GTCATTATTG	ACGTCAATGG	GCGGGGGTCG	TTGGGCGGTC

Fig. 10B

```
3001 AGCCAGGCGG GCCATTTACC GTAAGTTATG TAACGCGGAA CTCCATATAT GGGCTATGAA
3061 CTAATGACCC CGTAATTGAT TACTATTAAT AACTAGTCAA TAATCAATGT CAACATGGCG
3121 GTCATATTGG ACATGAGCCA ATATAAATGT ACATATTATG ATATAGATAC AACGTATGCA
3181 ATGGCCAATA GCCAATATTG ATTTATGCTA TATAACCAAT GACTAATATG GCTAATTGCC
3241 AATATTGATT CAATGTATAG ATCGATCTGG AAGGTGCTGA GGTACGATGA GACCCGCACC
3301 AGGTGCAGAC CCTGCGAGTG TGGCGGTAAA CATATTAGGA ACCAGCCTGT GATGCTGGAT
3361 GTGACCGAGG AGCTGAGGCC CGATCACTTG GTGCTGGCCT GCACCCGCGC TGAGTTTGGC
3421 TCTAGCGATG AAGATACAGA TTGAGGTACT GAAATGTGTG GGCGTGGCTT AAGGGTGGGA
3481 AAGAATATAT AAGGTGGGGG TCTTATGTAG TTTTGTATCT GTTTTGCAGC AGCCGCCGCC
3541 GCCATGAGCA CCAACTCGTT TGATGGAAGC ATTGTGAGCT CATATTTGAC AACGCGCATG
3601 CCCCCATGGG CCGGGGTGCG TCAGAATGTG ATGGGCTCCA GCATTGATGG TCGCCCCGTC
3661 CTGCCCGCAA ACTCTACTAC CTTGACCTAC GAGACCGTGT CTGGAACGCC GTTGGAGACT
3721 GCAGCCTCCG CCGCCGCTTC AGCCGCTGCA GCCACCGCCC GCGGGATTGT GACTGACTTT
3781 GCTTTCCTGA GCCCGCTTGC AAGCAGTGCA GCTTCCCGTT CATCCGCCCG CGATGACAAG
3841 TTGACGGCTC TTTTGGCACA ATTGGATTCT TTGACCCGGG AACTTAATGT CGTTTCTCAG
3901 CAGCTGTTGG ATCTGCGCCA GCAGGTTTCT GCCCTGAAGG CTTCCTCCCC TCCCAATGCG
3961 GTTTAAAACA TAAATAAAAA ACCAGACTCT GTTTGGATTT GGATCAAGCA AGTGTCTTGC
4021 TGTCTTTATT TAGGGGTTTT GCGCGCGCGG TAGGCCCGGG ACCAGCGGTC TCGGTCGTTG
4081 AGGGTCCTGT GTATTTTTTC CAGGACGTGG TAAAGGTGAC TCTGGATGTT CAGATACATG
4141 GGCATAAGCC CGTCTCTGGG GTGGAGGTAG CACCACTGCA GAGCTTCATG CTGCGGGGTG
4201 GTGTTGTAGA TGATCCAGTC GTAGCAGGAG CGCTGGGCGT GGTGCCTAAA AATGTCTTTC
4261 AGTAGCAAGC TGATTGCCAG GGGCAGGCCC TTGGTGTAAG TGTTTACAAA GCGGTTAAGC
4321 TGGGATGGGT GCATACGTGG GGATATGAGA TGCATCTTGG ACTGTATTTT TAGGTTGGCT
4381 ATGTTCCCAG CCATATCCCT CCGGGGATTC ATGTTGTGCA GAACCACCAG CACAGTGTAT
4441 CCGGTGCACT TGGGAAATTT GTCATGTAGC TTAGAAGGAA ATGCGTGGAA GAACTTGGAG
```

Fig. 10C

4501 ACGCCCTTGT GACCTCCAAG ATTTTCCATG CATTCGTCCA TAATGATGGC AATGGGCCCA
4561 CGGGCGGCGG CCTGGGCGAA GATATTTCTG GGATCACTAA CGTCATAGTT GTGTTCCAGG
4621 ATGAGATCGT CATAGGCCAT TTTTACAAAG CGCGGGCGGA GGGTGCCAGA CTGCGGTATA
4681 ATGGTTCCAT CCGGCCCAGG GGCGTAGTTA CCCTCACAGA TTTGCATTTC CCACGCTTTG
4741 AGTTCAGATG GGGGGATCAT GTCTACCTGC GGGGCGATGA AGAAAACGGT TTCCGGGGTA
4801 GGGGAGATCA GCTGGGAAGA AAGCAGGTTC CTGAGCAGCT GCGACTTACC GCAGCCGGTG
4861 GGCCCGTAAA TCACACCTAT TACCGGGTGC AACTGGTAGT TAAGAGAGCT GCAGCTGCCG
4921 TCATCCCTGA GCAGGGGGGC CACTTCGTTA AGCATGTCCC TGACTCGCAT GTTTTCCCTG
4981 ACCAAATCCG CCAGAAGGCG CTCGCCGCCC AGCGATAGCA GTTCTTGCAA GGAAGCAAAG
5041 TTTTTCAACG GTTTGAGACC GTCCGCCGTA GGCATGCTTT TGAGCGTTTG ACCAAGCAGT
5101 TCCAGGCGGT CCCACAGCTC GGTCACCTGC TCTACGGCAT CTCGATCCAG CATATCTCCT
5161 CGTTTCGCGG GTTGGGGCGG CTTTCGCTGT ACGGCAGTAG TCGGTGCTCG TCCAGACGGG
5221 CCAGGGTCAT GTCTTTCCAC GGGCGCAGGG TCCTCGTCAG CGTAGTCTGG GTCACGGTGA
5281 AGGGGTGCGC TCCGGGCTGC GCGCTGGCCA GGGTGCGCTT GAGGCTGGTC CTGCTGGTGC
5341 TGAAGCGCTG CCGGTCTTCG CCCTGCGCGT CGGCCAGGTA GCATTTGACC ATGGTGTCAT
5401 AGTCCAGCCC CTCCGCGGCG TGGCCCTTGG CGCGCAGCTT GCCCTTGGAG GAGGCGCCGC
5461 ACGAGGGGCA GTGCAGACTT TTGAGGGCGT AGAGCTTGGG CGCGAGAAAT ACCGATTCCG
5521 GGGAGTAGGC ATCCGCGCCG CAGGCCCCGC AGACGGTCTC GCATTCCACG AGCCAGGTGA
5581 GCTCTGGCCG TTCGGGGTCA AAAACCAGGT TTCCCCCATG CTTTTTGATG CGTTTCTTAC
5641 CTCTGGTTTC CATGAGCCGG TGTCCACGCT CGGTGACGAA AAGGCTGTCC GTGTCCCCGT
5701 ATACAGACTT GAGAGGCCTG TCCTCGACCG ATGCCCTTGA GAGCCTTCAA CCCAGTCAGC
5761 TCCTTCCGGT GGGCGCGGGG CATGACTATC GTCGCCGCAC TTATGACTGT CTTCTTTATC
5821 ATGCAACTCG TAGGACAGGT GCCGGCAGCG CTCTGGGTCA TTTTCGGCGA GGACCGCTTT
5881 CGCTGGAGCG CGACGATGAT CGGCCTGTCG CTTGCGGTAT TCGGAATCTT GCACGCCCTC
5941 GCTCAAGCCT TCGTCACTGG TCCCGCCACC AAACGTTTCG GCGAGAAGCA GGCCATTATC

Fig. 10D

```
6001 GCCGGCATGG CGGCCGACGC GCTGGGCTAC GTCTTGCTGG CGTTCGCGAC GCGAGGCTGG
6061 ATGGCCTTCC CCATTATGAT TCTTCTCGCT TCCGGCGGCA TCGGGATGCC CGCGTTGCAG
6121 GCCATGCTGT CCAGGCAGGT AGATGACGAC CATCAGGGAC AGCTTCAAGG ATCGCTCGCG
6181 GCTCTTACCA GCTGAGCAAA AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG
6241 CTGGCGTTTT TCCATAGGCT CCGCCCCCCT GACGAGCATC ACAAAAATCG ACGCTCAAGT
6301 CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAGCTCC
6361 CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC CTTTCTCCCT
6421 TCGGGAAGCG TGGCGCTTTC TCAATGCTCA CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC
6481 GTTCGCTCCA AGCTGGGCTG TGTGCACGAA CCCCCCGTTC AGCCCGACCG CTGCGCCTTA
6541 TCCGGTAACT ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA
6601 GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG
6661 TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC TCTGCTGAAG
6721 CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG GCAAACAAAC CACCGCTGGT
6781 AGCGGTGGTT TTTTTGTTTG CAAGCAGCAG ATTACGCGCA GAAAAAAAGG ATCTCAAGAA
6841 GATCCTTTGA TCTTTTCTAC GGGGTCTGAC GCTCAGTGGA ACGAAAACTC ACGTTAAGGG
6901 ATTTTGGTCA TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA
6961 AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA CCAATGCTTA
7021 ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT CATCCATAGT TGCCTGACTC
7081 CCCGTCGTGT AGATAACTAC GATACGGGAG GGCTTACCAT CTGGCCCCAG TGCTGCAATG
7141 ATACCGCGAG ACCCACGCTC ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA
7201 AGGGCCGAGC GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT
7261 TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT TGTTGCCATT
7321 GCTGCAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG CTCCGGTTCC
7381 CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC
7441 GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTTATGGCA
```

Fig. 10E

```
7501 GCACTGCATA ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG
7561 TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC TTGCCCGGCG
7621 TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT CATTGGAAAA
7681 CGTTCTTCGG GGCGAAAACT CTCAAGGATC TTACCGCTGT TGAGATCCAG TTCGATGTAA
7741 CCCACTCGTG CACCCAACTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA
7801 GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA
7861 ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA TTGTCTCATG
7921 AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA TAGGGGTTCC GCGCACATTT
7981 CCCCGAAAAG TGCCACCTGA CGTCTAAGAA ACCATTATTA TCATGACATT AACCTATAAA
8041 AATAGGCGTA TCACGAGGCC CTTTCGTCTT CAA
```

Fig. 10F

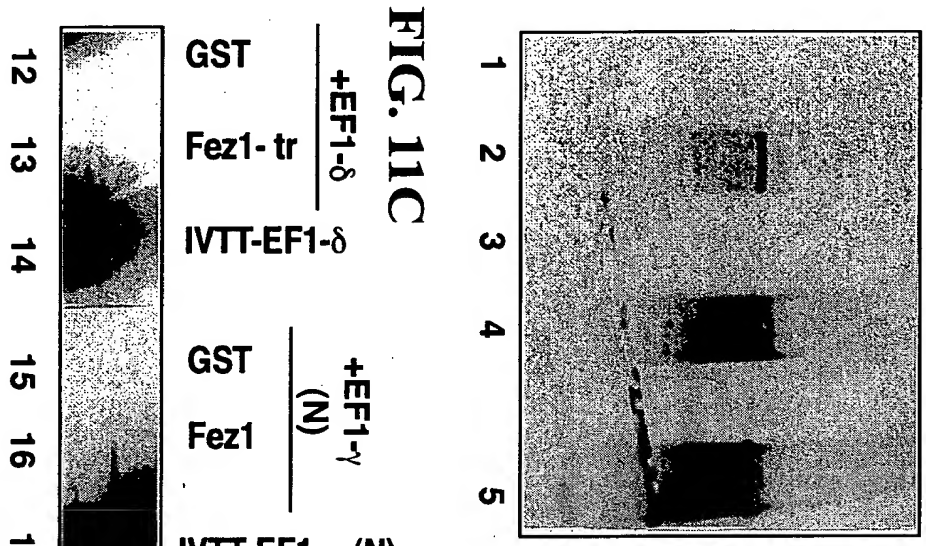


FIG. 11A

FIG. 11B

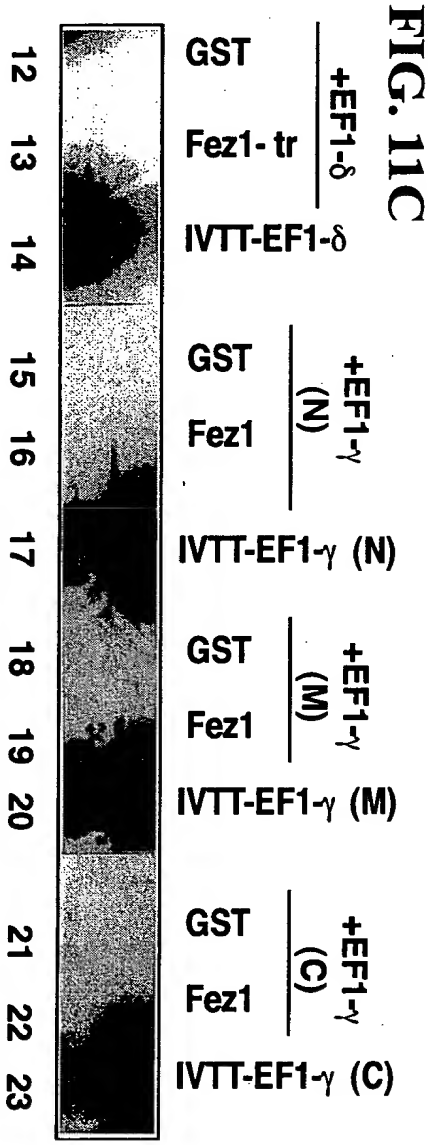


FIG. 11C

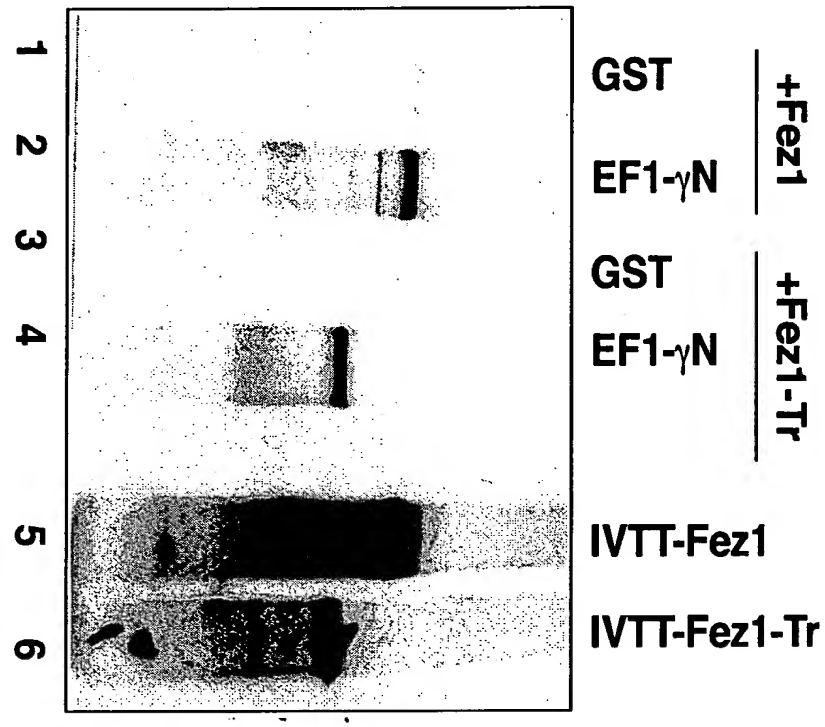

1
2
3
4
5
6
GST
EF1-γN
GST
EF1-γN
+Fez1
+Fez1-Tr
IVTT-Fez1
IVTT-Fez1-Tr

FIG. 12

FIG. 13

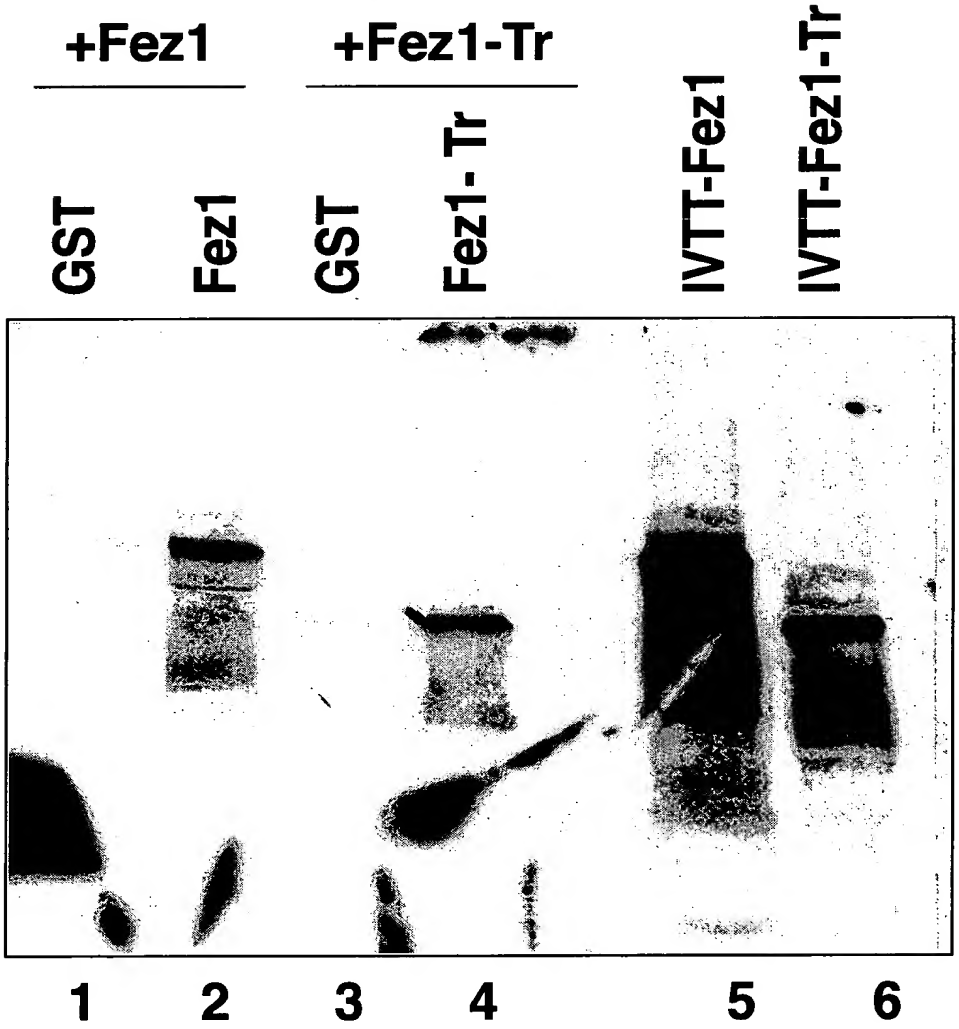

+Fez1
+Fez1-Tr
GST
Fez1
GST
Fez1- Tr
IVTT-Fez1
IVTT-Fez1-Tr
1
2
3
4
5
6

FIG. 14A

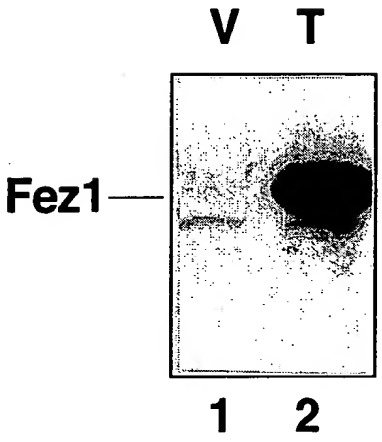


FIG. 14B

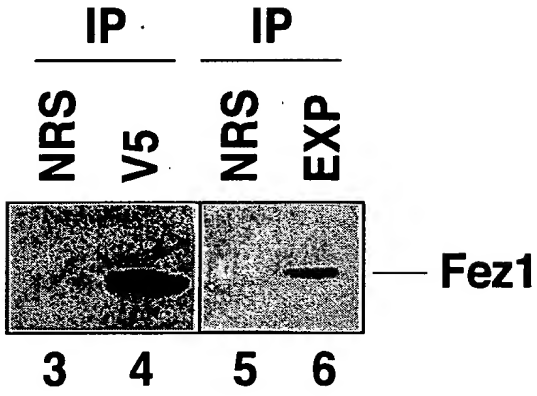


FIG. 14C

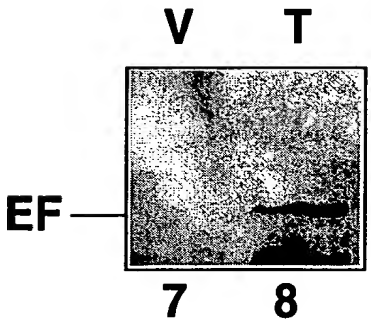


FIG. 14D

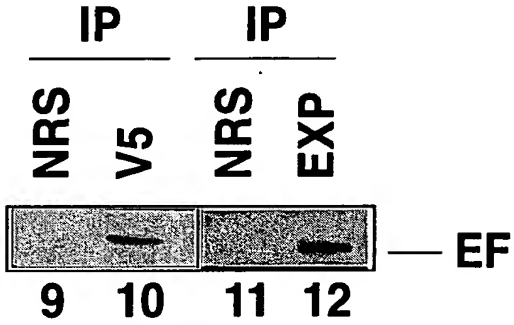


FIG. 15B

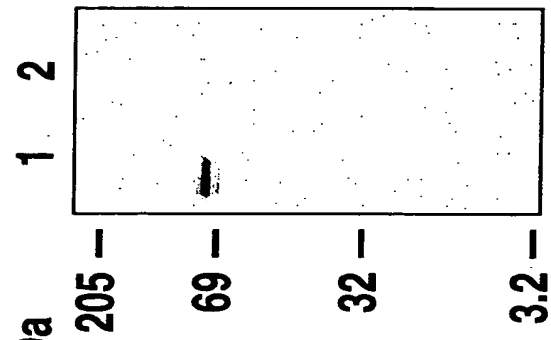


FIG. 15A

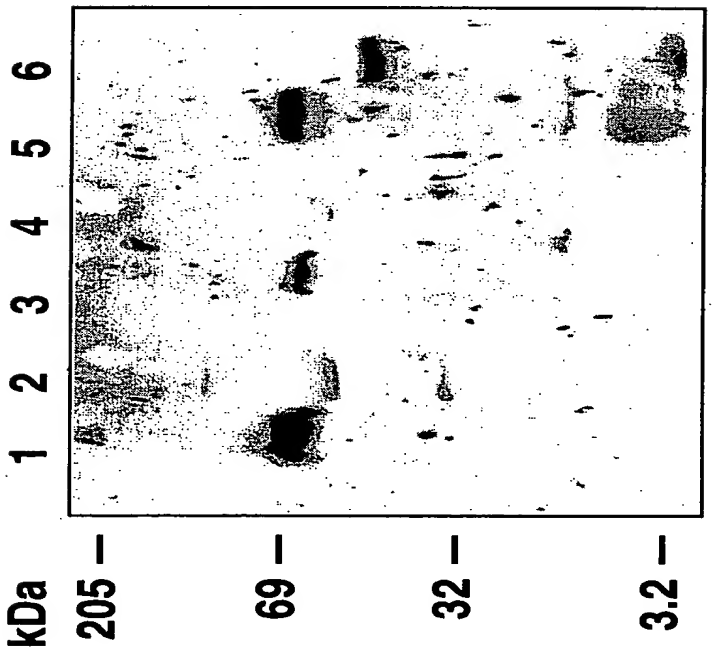


FIG. 16A

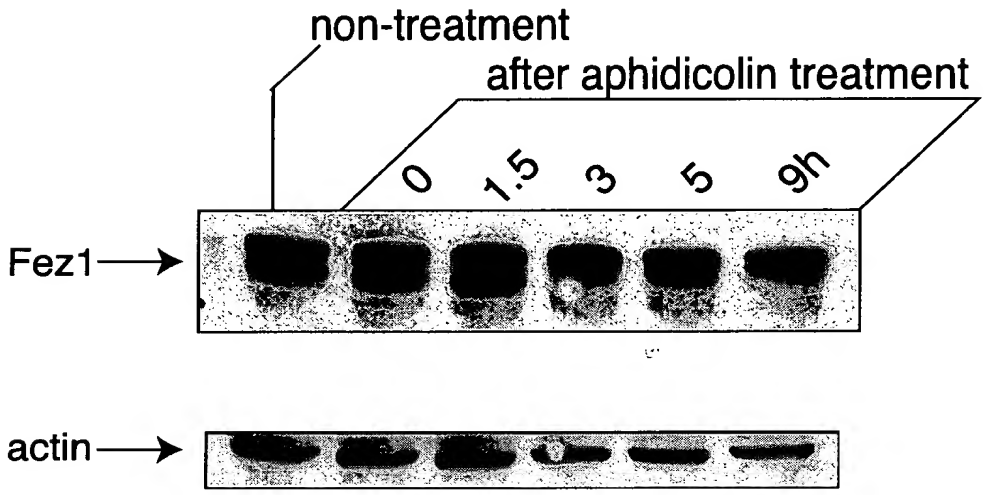
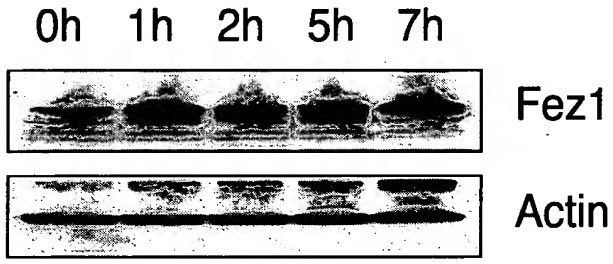


FIG. 16B



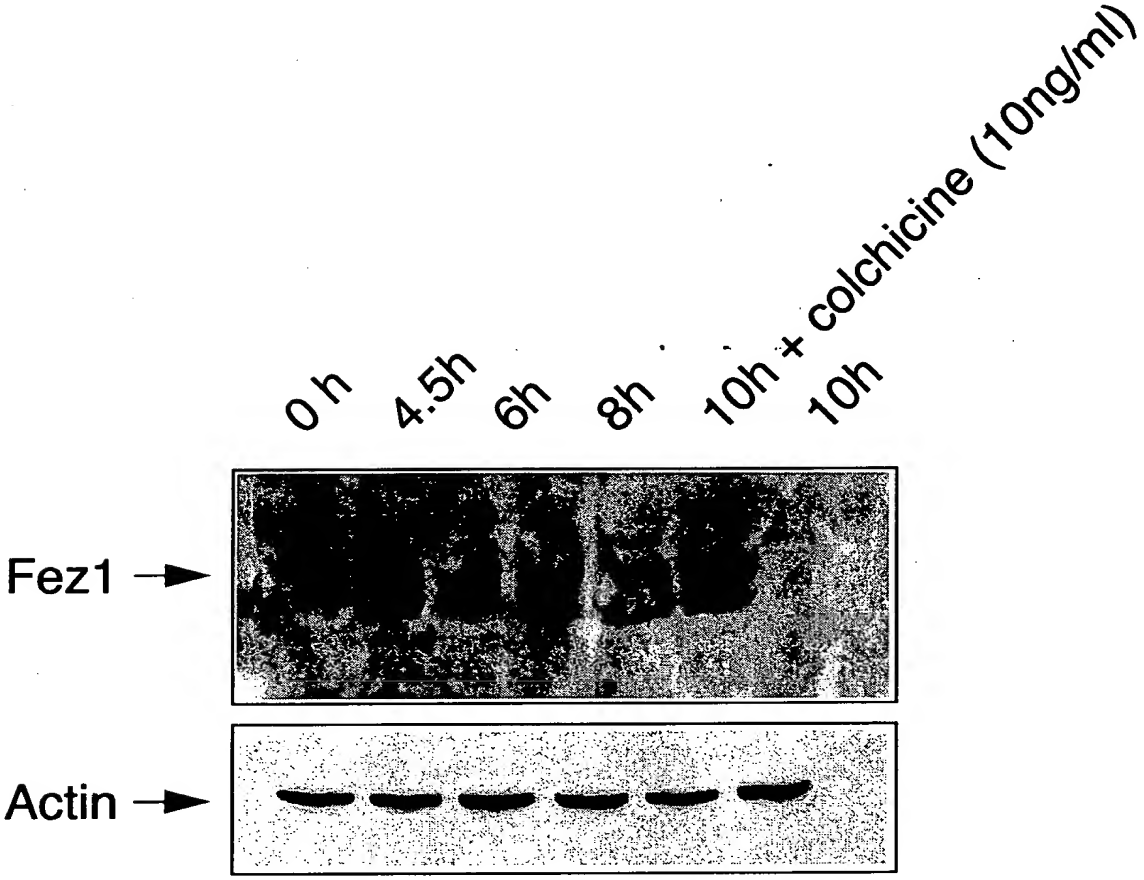


FIG. 17

FIG. 18

FIG. 19

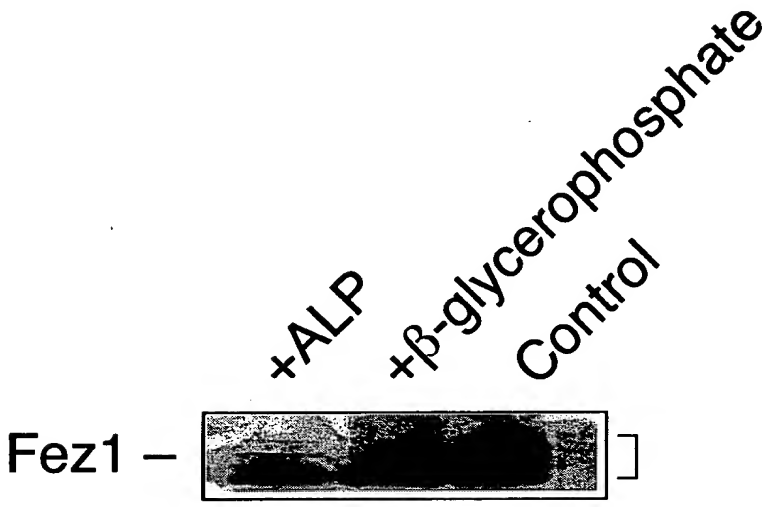
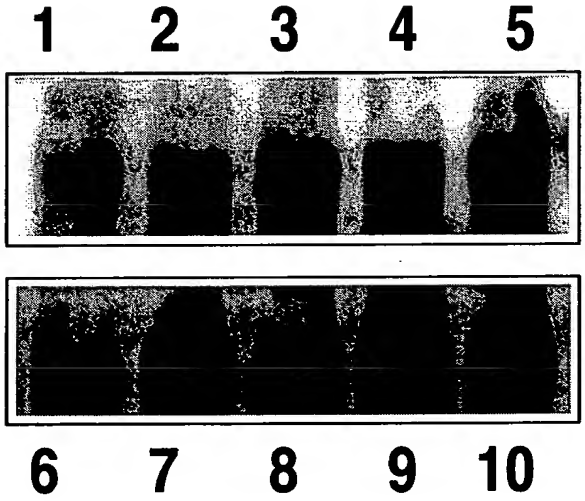


FIG. 20



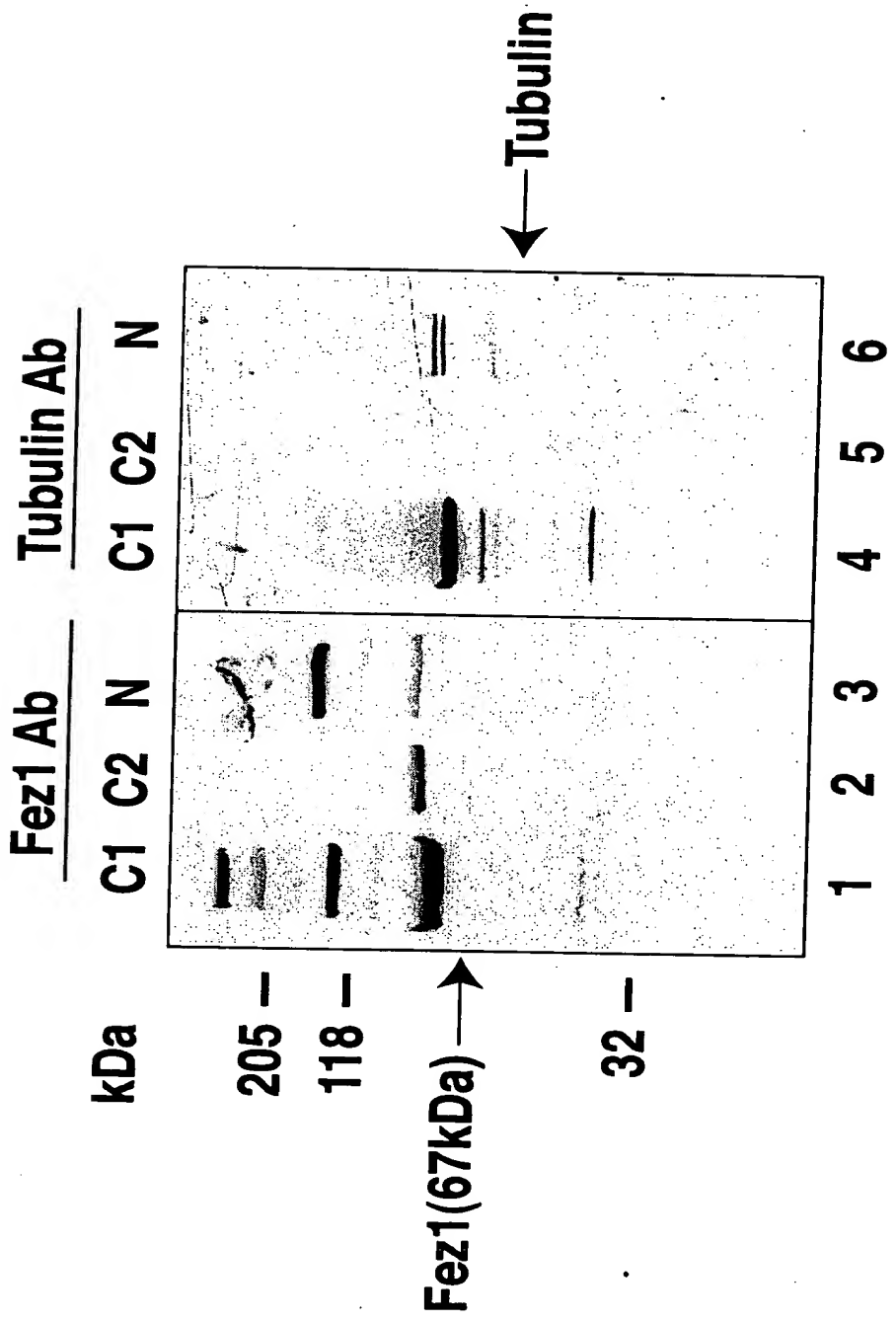
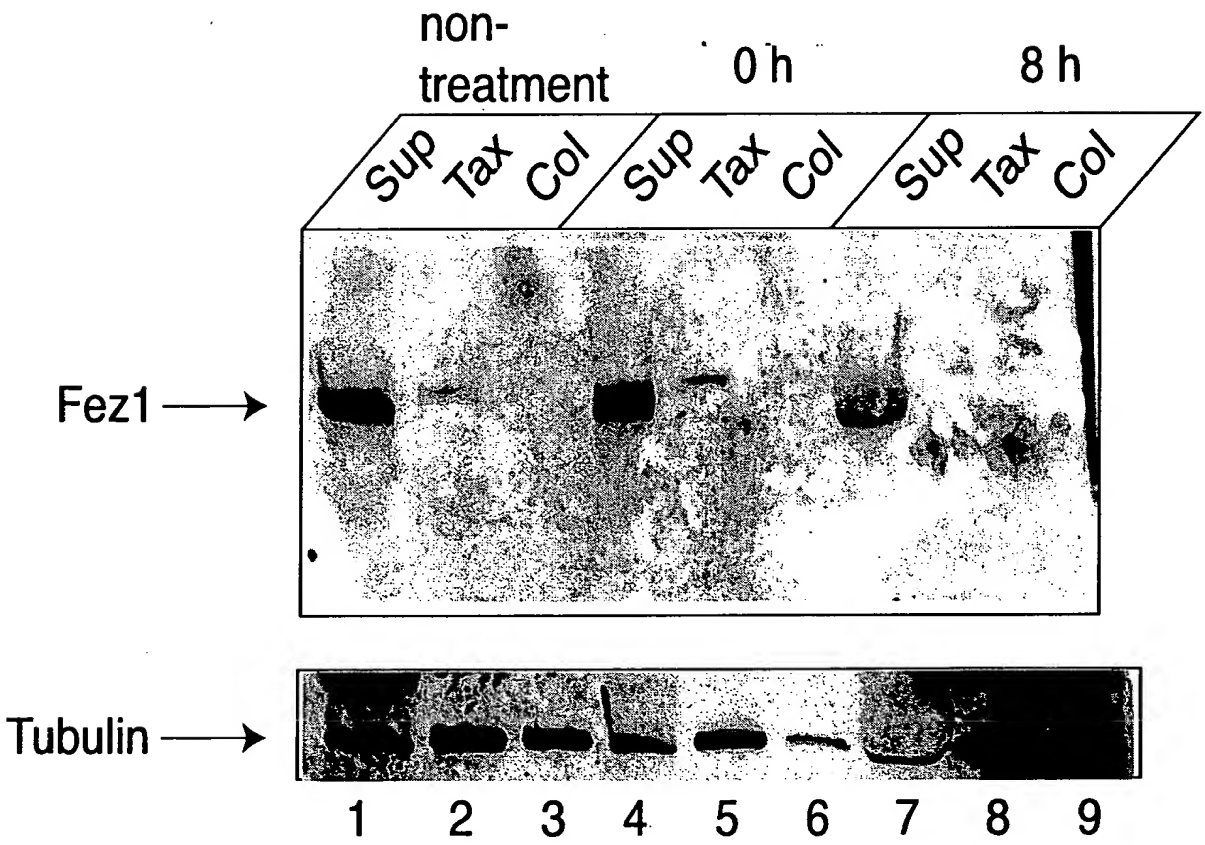

Tubulin
Tubulin Ab
Fez1 Ab
C1 C2 N
C1 C2 N
1 2 3 4 5 6
kDa
205
118
32
Fez1(67kDa)

FIG. 21

FIG. 22


non-
treatment
0 h
8 h
Sup
Tax
Col
Sup
Tax
Col
Sup
Tax
Col
Fez1
Tubulin
1
2
3
4
5
6
7
8
9

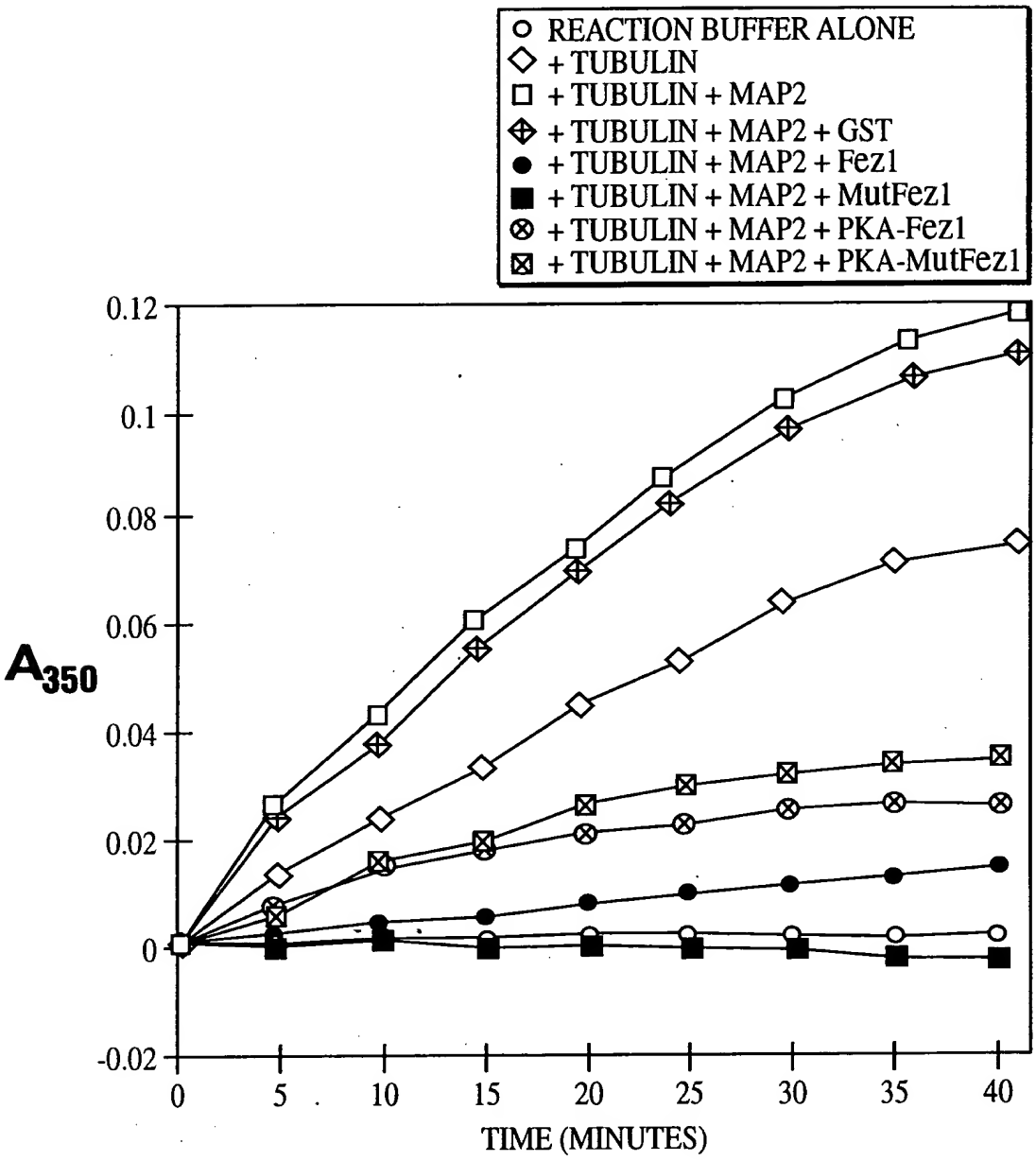

REACTION BUFFER ALONE
+ TUBULIN
+ TUBULIN + MAP2
+ TUBULIN + MAP2 + GST
+ TUBULIN + MAP2 + Fez1
+ TUBULIN + MAP2 + MutFez1
+ TUBULIN + MAP2 + PKA-Fez1
+ TUBULIN + MAP2 + PKA-MutFez1
A350
0.12
0.1
0.08
0.06
0.04
0.02
0
-0.02
0
5
10
15
20
25
30
35
40
TIME (MINUTES)

Fig. 23